



QY 61 ELLLLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAAE 120  
|||||  
Db 61 ELLLLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAAE 120  
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QY 121 LGRDVARYLRAAAGTRGSNHARIDAAEGPSDIPD 156  
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Db 121 LGRDVARYLRAAAGTRGSNHARIDAAEGPSDIPD 156  
|||||

## RESULT 2

US-08-306-511A-2

; Sequence 2, Application US/08306511A

; Patent No. 5962316

; GENERAL INFORMATION:

; APPLICANT: Beach, David H.

; APPLICANT: Demetrick, Douglas J.

; APPLICANT: Serrano, Manuel

; APPLICANT: Hannon, Gregory J.

; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses

; TITLE OF INVENTION: Related Thereto

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE &amp; COCKFIELD

; STREET: 60 State Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII(text)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/306.511A

; FILING DATE: 14-SEP-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Vincent, Matthew P.

; REGISTRATION NUMBER: 36,709

; REFERENCE/DOCKET NUMBER: CSI-001CP2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 227-7400

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 156 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-306-511A-2

Query Match 100.0%; Score 156; DB 2; Length 156;  
Best Local Similarity 100.0%; Pred. No. 8.7e-138;  
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPAAAGSSMEPSADWLATAAARGVEEVRALLEVALPNAFNSYGRPRPIQVMMGSRVA 60  
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Db 1 MDPAAAGSSMEPSADWLATAAARGVEEVRALLEVALPNAFNSYGRPRPIQVMMGSRVA 60  
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QY 61 ELLLLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAAE 120  
|||||

Db 61 ELLLLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAAE 120  
|||||

QY 121 LGRDVARYLRAAAGTRGSNHARIDAAEGPSDIPD 156  
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Db 121 LGRDVARYLRAAAGTRGSNHARIDAAEGPSDIPD 156  
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RESULT 3

US-08-893-274-2

; Sequence 2, Application US/08893274

; Patent No. 5968821  
; GENERAL INFORMATION:  
; APPLICANT: Beach, David H.  
; APPLICANT: Demetrick, Douglas J.  
; APPLICANT: Serrano, Manuel  
; APPLICANT: Hannon, Gregory J.  
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins,  
; TITLE OF INVENTION: and Uses Related Thereto  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
; STREET: One Post Office Square  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII(text)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/893.274

; FILING DATE: 15-JULY-1997

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/306,511

; FILING DATE: 14-SEPTEMBER-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/248,812

; FILING DATE: 25-MAY-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/227,371

; FILING DATE: 14-APRIL-1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/154,915

; FILING DATE: 18-NOVEMBER-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/991,997

; FILING DATE: 17-DECEMBER-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/963,308

; FILING DATE: 16-OCTOBER-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Vincent, Matthew P.

; REGISTRATION NUMBER: 36,709

; REFERENCE/DOCKET NUMBER: MIV-071.09

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 832-1000

; TELEFAX: (617) 832-7000

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 156 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-893-274-2

Query Match 100.0%; Score 156; DB 2; Length 156;  
Best Local Similarity 100.0%; Pred. No. 8.7e-138;  
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPAAAGSSMEPSADWLATAAARGVEEVRALLEVALPNAFNSYGRPRPIQVMMGSRVA 60  
|||||

Db 1 MDPAAAGSSMEPSADWLATAAARGVEEVRALLEVALPNAFNSYGRPRPIQVMMGSRVA 60  
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QY 61 ELLLLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAAE 120  
|||||

Db 61 ELLLLHGAEPNCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAAE 120  
|||||

QY 121 LGRDVARYLRAAAGTRGSNHARIDAAEGPSDIPD 156  
|||||

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OM protein - protein search, using sw model

Run on: October 31, 2001, 07:10:53 ; Search time 14.49 Seconds  
(without alignments)  
820.099 Million cell updates/sec

Title: US-09-016-869A-2  
Perfect score: 156  
Sequence: 1 MDPAGSSMEPSADWLATRA.....TRGSNHARIDAAEGPSDIPD 156

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 219241 seqs, 76174552 residues

size : 0  
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR\_68: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	121	77.6	JF0141	cyclin dependent k
2	72	46.2	B55479	CDK4 inhibitor p14
3	48	30.8	I78845	p15INK4b - mouse
4	34	21.8	I52720	gene p15INK4B prot
5	19	12.2	I58352	p16INK4a - mouse
6	8	5.1	G69303	iron (III) ABC tra
7	8	5.1	T43647	hypothetical prote
8	8	5.1	A44212	genome polyprotein
9	8	5.1	MMWHRG	hypothetical prote
10	7	4.5	B27683	hypothetical prote
11	7	4.5	A70792	ORF3 protein - Orf
12	7	4.5	E34768	cyclin-dependent k
13	7	4.5	A57378	CDK4/Cdk6 inhibito
14	7	4.5	A57379	cyclin-dependent k
15	7	4.5	B57378	probable nicotinam
16	7	4.5	T36141	alcohol dehydrogen
17	7	4.5	B3724	alcohol dehydrogen
18	7	4.5	C23724	alcohol dehydrogen
19	7	4.5	D23724	alcohol dehydrogen
20	7	4.5	A75304	ABC transporter, A
21	7	4.5	D29880	probable enoyl-CoA
22	7	4.5	D69980	purine nucleoside
23	7	4.5	F82977	transcription regu
24	7	4.5	D8FEFL	alcohol dehydrogen
25	7	4.5	A40553	alcohol dehydrogen
26	7	4.5	S15711	alcohol dehydrogen
27	7	4.5	S15712	alcohol dehydrogen
28	7	4.5	S06001	alcohol dehydrogen
29	7	4.5	B24268	alcohol dehydrogen

30	7	4.5	254	1	A24268	alcohol dehydrogen
31	7	4.5	254	1	S01901	alcohol dehydrogen
32	7	4.5	254	1	E23724	alcohol dehydrogen
33	7	4.5	254	2	A23724	alcohol dehydrogen
34	7	4.5	254	2	D72464	hypothetical prote
35	7	4.5	273	2	T34740	hypothetical prote
36	7	4.5	283	2	E84258	hypothetical prote
37	7	4.5	314	2	D70313	riboflavin kinase
38	7	4.5	318	1	F70536	3',5'-cyclic-nucle
39	7	4.5	331	2	D86413	probable cysteine
40	7	4.5	334	2	A82751	ABC transporter AT
41	7	4.5	345	2	B84752	probable cysteine
42	7	4.5	346	2	C86413	probable cysteine
43	7	4.5	348	2	T18230	alcohol dehydrogen
44	7	4.5	348	2	T35450	ABC transporter AT
45	7	4.5	353	2	D75553	branched-chain ami

ALIGNMENTS

RESULT 1

JE0141  
cyclin dependent kinase inhibitor - human  
N:Alternate names: CDK4 inhibitor p16(INK4A/MTS1); cyclin-dependent kinase inhibitor  
C:Species: Homo sapiens (man)  
C>Date: 02-Jun-1998 #sequence.revision 10-Jul-1998 #text\_change 19-May-2000  
C:Accession: JE0141; I59268; S39359; I59585; JC5679  
R:Huang, C.G.; Deng, W.; Fu, J.L.  
Chin. J. Biotechnol. 13, 105-107, 1997  
A:Title: Molecular cloning and sequencing of p16 ink4 cDNA from hela cell.  
A:Reference number: JE0141  
A:Accession: JE0141  
A:Molecule type: mRNA  
A:Residues: 1-156 <HUA>  
A:Experimental source: Hella cell  
R:Okamoto, A.; Demetrick, D.J.; Spillare, E.A.; Hagiwara, K.; Hussain, S.P.; Bennett,  
Proc. Natl. Acad. Sci. U.S.A. 91, 11045-11049, 1994  
A:Title: Mutations and altered expression of p16INK4 in human cancer.  
A:Reference number: I59268; MUID:95062202  
A:Accession: I59268  
A>Status: translation not shown; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-152 <OKA>  
A:Cross-references: GB:I27211; NID:g558656; PIDN:AAA92554.1; PID:g558657  
A:Note: the sequence is revised in GenBank entry HOMINK4X, release 113.0, PIDN:AAA925  
R:Serrano, M.; Hannon, G.J.; Beach, D.  
Nature 366, 704-707, 1993  
A:Title: A new regulatory motif in cell-cycle control causing specific inhibition of  
A:Reference number: S39359; MUID:94081956  
A:Accession: S39359  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 9-34, 'V', 36-156 <SER>  
A:Note: this sequence is corrected in reference I59268  
R:Kamb, A.; Gruis, N.A.; Weaver-Feldhaus, J.; Liu, Q.; Harshman, K.; Tavtigian, S.V.;  
Science 264, 436-440, 1994  
A:Title: A cell cycle regulator potentially involved in genesis of many tumor types.  
A:Reference number: I59585; MUID:94204645  
A:Accession: I59585  
A>Status: translation not shown; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 51-152 <KAM>  
A:Cross-references: GB:S69804; NID:g546272; PIDN:AAD14048.1; PID:g4261748  
C:Comment: This protein inhibits the activity of cyclin D1/CDK4 and cyclin D1/CDK6 ki  
C:Genetics:  
A:Gene: GDB:CDKN2A; CDK4I; MLM; p16; INK4; MTS1; CMM2; CDKN2  
A:Cross-references: GDB:353562; OMIM:600160  
A:Map position: 9p21-9p21  
C:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homol  
C:Keywords: cell cycle control; protein kinase inhibitor; tumor suppressor



Result No.	Query No.	Score	%		Length	DB	ID	Description
			Match					
1	1	121	77.6	156	1	CDN2_HUMAN	P42771	homo sapien
2	2	72	46.2	138	1	CDN5_HUMAN	P42772	homo sapien
3	4	48	30.8	130	1	CDN5_MOUSE	P55271	mus musculus
4	4	36	23.1	130	1	CDN5_RAT	P55272	rattus norv
5	5	19	12.2	167	1	CDN2_MOUSE	P51480	mus musculus
6	6	14	9.0	171	1	CDN2_MONDO	077617	monodelphis
7	7	8	5.1	1691	1	POLN_HEVME	Q03495	hepatitis e
8	8	8	5.1	1693	1	POLN_HEVBU	P29324	hepatitis e
9	9	8	5.1	1693	1	POLN_HEVHY	P29324	hepatitis e
10	10	8	5.1	1693	1	POLN_HEVPA	Q04610	hepatitis e
11	11	7	4.5	166	1	CDN7_HUMAN	P33424	hepatitis e
12	12	7	4.5	166	1	CDN7_MOUSE	P55273	homo sapien
13	13	7	4.5	218	1	GPR_BACSH	Q60773	mus musculus
14	14	7	4.5	231	1	MPN_BACSU	P95650	rhodobacter
15	15	7	4.5	253	1	ADH1_DROHY	032028	bacillus su
16	16	7	4.5	253	1	ADH1_DROMT	P23236	drosophila
17	17	7	4.5	253	1	ADH1_DROMU	P22246	drosophila
18	18	7	4.5	253	1	ADH1_DRONA	P07161	drosophila
19	19	7	4.5	253	1	ADH2_DROAR	P12854	drosophila
20	20	7	4.5	253	1	ADH2_DROBU	P27581	drosophila
21	21	7	4.5	253	1	ADH2_DROHY	P25720	drosophila
22	22	7	4.5	253	1	ADH2_DROMO	P23237	drosophila
23	23	7	4.5	253	1	ADH2_DROMU	P09369	drosophila
24	24	7	4.5	253	1	ADH2_DROMY	P07160	drosophila
25	25	7	4.5	253	1	ADH2_DROWH	P25721	drosophila
26	26	7	4.5	253	1	ADH_DROAD	P4267	drosophila
27	27	7	4.5	253	1	ADH_DROAF	Q00669	drosophila
28	28	7	4.5	253	1	ADH_DRODI	P21518	drosophila
29	29	7	4.5	253	1	ADH_DROGR	P22245	drosophila
30	30	7	4.5	253	1	ADH_DROHA	P51551	drosophila
31	31	7	4.5	253	1	ADH_DROHE	P51549	drosophila
32	32	7	4.5	253	1	ADH_DROWM	P21898	drosophila
33	33	7	4.5	253	1	ADH_DRONI	Q00671	drosophila

[7] VARIANTS NON-SMALL CELL LUNG CARCINOMAS (NSCLC).  
 RP MEDLINE=94338359; PubMed=8060323;  
 RA Hayashi N., Sugimoto Y., Tsuchiya E., Ogawa M., Nakamura Y.;  
 RT "Somatic mutations of the MTS (multiple tumor suppressor) 1/CDK41  
 cell lung carcinomas.";  
 RL Biochem. Biophys. Res. Commun. 202:1426-1430(1994).  
 [8]  
 RP VARIANTS MELANOMA THR-49; SER-71; PRO-87; TRP-101; ASP-126 & THR-148.  
 RX MEDLINE=95078916; PubMed=7987387;  
 RA Hussussian C.J., Struwing J.P., Goldstein A.M., Higgins P.A.T.,  
 RA Ally D.S., Sheahan M.D., Clark W.H. Jr., Tucker M.A., Dracopoli N.C.;  
 RT "Germline p16 mutations in familial melanoma.";  
 RL Nat. Genet. 8:15-21(1994).  
 [9]  
 RP VARIANTS SQUAMOUS CELL CARCINOMA (SCCA) SER-127 AND CYS-144.  
 RX MEDLINE=95060835; PubMed=7970734;  
 RA Zhou X., Tarmir L., Yin J., Jiang H.-Y., Suzuki H., Rhyu M.-G.,  
 RA Abraham J.M., Meltzer S.J.;  
 RT "The MTS1 gene is frequently mutated in primary human esophageal  
 tumors.";  
 RL Oncogene 9:3737-3741(1994).  
 [10]  
 RP VARIANTS.  
 RX MEDLINE=95188190; PubMed=7882351;  
 RA Okamoto A., Hussain S.P., Hagiwara K., Spillare E.A., Rusin M.R.,  
 RA Demetrick D.J., Serrano M., Hannon G.J., Shiseki M., Zariwala M.,  
 RA Bennett W.P., Forrester K., Gerwin B., Beach D.H., Harris C.C.;  
 RT "Mutations in the p16INK4/MTS1/CDKN2, p15INK4B/MTS2, and p18 genes in  
 primary and metastatic lung cancer.";  
 RL Cancer Res. 55:1448-1451(1995).  
 [11]  
 RP VARIANTS MELANOMA P-32; A-35; E-35; R-50; I-53, AND VARIANT T-148.  
 RX MEDLINE=96121580; PubMed=8595405;  
 RA Walker G.J., Hussussian C.J., Flores J.F., Glendening J.M.,  
 RA Haluska F.G., Dracopoli N.C., Hayward N.K., Fountain J.W.;  
 RT "Mutations of the CDKN2/p16INK4 gene in Australian melanoma  
 kindreds.";  
 RL Hum. Mol. Genet. 4:1845-1852(1995).  
 [12]  
 RP CHARACTERIZATION OF VAR. T-49; S-71; L-81; P-87; W-101; D-126 & T-148.  
 RX MEDLINE=95375774; PubMed=7647780;  
 RA Ranade K., Hussussian C.J., Sikorski R.S., Varmus H.E.,  
 RA Goldstein A.M., Tucker M.A., Serrano M., Hannon G.J., Beach D.,  
 RA Dracopoli N.C.;  
 RT "Mutations associated with familial melanoma impair p16INK4  
 function.";  
 RL Nat. Genet. 10:114-116(1995).  
 [13]  
 RP VARIANTS MELANOMA I-53 AND C-107, AND VARIANTS V-68; T-85 AND T-148.  
 RX MEDLINE=96323259; PubMed=8710906;  
 RA Fitzgerald M.G., Harkin D.P., Silva-Arrieta S., Macdonald D.J.,  
 RA Luchina L.C., Unsal H., O'Neill E., Koh J., Finkelstein D.M.,  
 RA Isselbacher K.J., Sober A.J., Haber D.A.;  
 RT "Prevalence of germline mutations in p16, p19ARF, and CDK4 in  
 familial melanoma: analysis of a clinic-based population.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 93:8541-8545(1996).  
 [14]  
 RP VARIANTS MELANOMA PRO-24; ILE-53 AND THR-118, AND VARIANT THR-148.  
 RX MEDLINE=97472457; PubMed=9328469;  
 RA Harland M., Meloni R., Gruis N., Pinney E., Brookes S., Spurr N.K.,  
 RA Frischauf A.-M., Bataille V., Peters G., Cuzick J., Selby P.,  
 RA Bishop D.T., Bishop J.N.;  
 RT "Germline mutations of the CDKN2 gene in UK melanoma families.";  
 RL Hum. Mol. Genet. 6:2061-2067(1997).  
 [15]  
 RP VARIANTS FAMILIAL MELANOMA.  
 RX MEDLINE=98087572; PubMed=9425228;  
 RA Soufir N., Avril M.-F., Chompret A., Demenais F., Bombled J.,  
 RA Spatz A., Stoppa-Lyonnet D., Benard J., Bressac-De Paillerets B.;  
 RT "Prevalence of p16 and CDK4 germline mutations in 48 melanoma-prone  
 families in France."

Hum. Mol. Genet. 7:209-216(1998).  
 [16]  
 RP ERYTHROCYTES.  
 RA Soufir N., Avril M.-F., Chompret A., Demenais F., Bombled J.,  
 RA Spatz A., Stoppa-Lyonnet D., Benard J., Bressac-De Paillerets B.;  
 RL Hum. Mol. Genet. 7:941-941(1998).  
 [17]  
 RP VARIANT PANCREATIC CARCINOMA CYS-146.  
 RA Moskaluk C.A., Hruban R.H., Lietman A., Smyrk T., Fusaro L.,  
 RA Fusaro R., Lynch J., Yeo C.J., Jackson C.E., Lynch H.T., Kern S.E.;  
 RT "Novel germline p16INK4 allele (Asp145Cys) in a family with multiple  
 pancreatic carcinomas.";  
 RL Hum. Mutat. 12:70-70(1998).  
 [18]  
 RP VARIANTS MELANOMA LEU-48; VAL-57; ASP-89 AND MET-117.  
 RA Gretsardottir S., Olafsdottir G.H., Borg A.;  
 RT "Five novel somatic CDKN2/p16 mutations identified in melanoma,  
 glioma and carcinoma of the pancreas.";  
 RL Hum. Mutat. 12:212-212(1998).  
 CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS ITS  
 CC REGULATOR OF THE PROLIFERATION OF NORMAL CELLS.  
 CC -1- SUBUNIT: HETERODIMER WITH CDK4 OR CDK6.  
 CC -1- DISEASE: CDKN2A MUTATIONS ARE INVOLVED IN TUMOR FORMATION IN A  
 CC WIDE RANGE OF TISSUES.  
 CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE  
 CC INHIBITORS.  
 CC -1- SIMILARITY: CONTAINS 4 ANK REPEATS.  
 CC -----  
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC use by non-profit institutions as long as its content is in no way  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; L27211; AAA92554.1; -;  
 DR EMBL; U12820; AAB60645.1; -;  
 DR EMBL; U12818; AAB60645.1; JOINED.  
 DR EMBL; U12819; AAB60645.1; JOINED.  
 DR EMBL; S69804; AAD14048.1; -;  
 DR EMBL; X94154; CAA63870.1; -;  
 DR PDB; 1BI7; 16-FEB-99.  
 DR MIM; 600160; -;  
 DR InterPro; IPR002110; -;  
 DR Pfam; PF00023; ank; 3.  
 DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
 KW Cell cycle; Anti-oncogene; Repeat; ANK repeat; Disease mutation;  
 KW Polymorphism; Li-Fraumeni syndrome; 3D-structure.  
 FT REPEAT 11 40 ANK 1.  
 FT REPEAT 44 72 ANK 2.  
 FT REPEAT 77 106 ANK 3.  
 FT REPEAT 110 139 ANK 4.  
 FT VARIANT 14 14 D -> E (IN A BILIARY TRACT TUMOR).  
 FT VARIANT 16 16 L -> P (IN A BILIARY TRACT TUMOR AND A  
 FT FAMILIAL MELANOMA).  
 FT FTTid=VAR\_001409.  
 FT A -> P (IN A LONG TUMOR AND MELANOMA).  
 FT FTTid=VAR\_001410.  
 FT A -> S (IN A BILIARY TRACT TUMOR).  
 FT FTTid=VAR\_001411.  
 FT G -> D (IN A PANCREAS TUMOR).  
 FT FTTid=VAR\_001412.  
 FT R -> C (IN MELANOMA).  
 FT FTTid=VAR\_001413.  
 FT R -> P (IN FAMILIAL MELANOMA AND  
 FT MELANOMA).  
 FT FTTid=VAR\_001414.  
 FT E -> D (IN A BILIARY TRACT TUMOR).  
 FT FTTid=VAR\_001415.  
 FT L -> P (IN FAMILIAL MELANOMA).

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OM protein - protein search, using sw model

Run on: October 31, 2001, 07:14:18 ; Search time 22.49 Seconds  
(without alignments)  
917.723 Million cell updates/sec

Title: US-09-016-869A-2  
Perfect score: 156  
Sequence: 1 MDPAGSMPEPSDWLATAA.....TRGSNHARIDAAEGPSDIPD 156

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 425026 seqs, 132305027 residues

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Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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- 1: sp\_archaea.\*
  - 2: sp\_bacteria.\*
  - 3: sp\_fungi.\*
  - 4: sp\_human.\*
  - 5: sp\_invertebrate.\*
  - 6: sp\_mammal.\*
  - 7: sp\_mhc.\*
  - 8: sp\_organelle.\*
  - 9: sp\_phage.\*
  - 10: sp\_plant.\*
  - 11: sp\_rodent.\*
  - 12: sp\_unclassified.\*
  - 13: sp\_vertebrate.\*
  - 14: sp\_virus.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	106	67.9	106	4	Q9np05
2	54	34.6	81	6	Q9gmf2
3	51	32.7	86	6	Q9xs52
4	51	32.7	102	6	Q9xs51
5	48	30.8	86	11	O54846
6	48	30.8	86	11	Q9z1c1
7	48	30.8	86	11	Q9oup0
8	47	30.1	103	6	Q9tsv1
9	32	20.5	36	4	O9upb7
10	32	20.5	116	4	O95440
11	26	16.7	86	6	Q9tsy0
12	19	12.2	112	11	Q9qwh4
13	19	12.2	113	11	Q9z1c2
14	19	12.2	159	11	Q9ro23
15	19	12.2	168	11	O89088
16	19	12.2	168	11	P97510
17	18	11.5	113	11	Q9qwh8
18	18	11.5	113	11	Q9qwh7
19	18	11.5	113	11	Q9qwh6

20	15	9.6	58	6	O97886	O97886 equus cabal
21	15	9.6	113	11	O9QWH5	O9qwh5 mus musculus
22	14	9.0	21	4	O9UD00	O9ud00 homo sapien
23	12	7.7	157	11	O9EQ33	O9eq33 mesocricetu
24	8	5.1	44	11	O9Z1C0	O9z1c0 mus musculus
25	8	5.1	44	11	O9QJ3	O9qj3 mus musculus
26	8	5.1	91	14	O9WLJ9	O9wlj9 hepatitis e
27	8	5.1	124	13	P70067	P70067 xiphophorus
28	8	5.1	124	13	O9W618	O9w618 xiphophorus
29	8	5.1	300	14	P89468	P89468 herpes simp
30	8	5.1	334	1	O29818	O29818 archaeoglob
31	8	5.1	390	3	O94237	O94237 schizosacch
32	8	5.1	452	14	O71145	O71145 hepatitis e
33	8	5.1	487	14	O81869	O81869 hepatitis e
34	8	5.1	727	14	O81873	O81873 hepatitis e
35	8	5.1	747	14	O9J513	O9j513 fowlpox vir
36	8	5.1	1050	4	O9H014	O9h014 homo sapien
37	8	5.1	1205	3	O9HEF5	O9hif5 schizosacch
38	8	5.1	1685	14	O9E8G6	O9e8g6 hepatitis e
39	8	5.1	1693	14	O69410	O69410 hepatitis e
40	8	5.1	1693	14	O81344	O81344 hepatitis e
41	8	5.1	1693	14	O81862	O81862 hepatitis e
42	8	5.1	1693	14	O89444	O89444 hepatitis e
43	8	5.1	1693	14	O81876	O81876 hepatitis e
44	8	5.1	1693	14	O39221	O39221 hepatitis e
45	8	5.1	1693	14	O9WLL5	O9wll5 hepatitis e

ALIGNMENTS

RESULT 1

Q9NP05 ID Q9NP05 PRELIMINARY; PRT; 106 AA.

AC Q9NP05;

DT 01-OCT-2000 (TREMREL. 15, Created)

DT 01-OCT-2000 (TREMREL. 15, Last sequence update)

DT 01-MAR-2001 (TREMREL. 16, Last annotation update)

DE CDK4I PROTEIN (FRAGMENT).

GN CDK4I.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=94203288; PubMed=8152487;

RA Nobori T., Miura K., Wu D.J., Lois A., Takabayashi K., Carson D.A.;

RT "Deletions of the cyclin-dependent kinase-4 inhibitor gene in multiple human cancers."

RL Nature 368:753-756(1994).

DR EMBL; S69824; AAD14050.1; .

DR EMBL; S69822; AAD14050.1; JOINED.

DR InterPro; IPR002110; .

DR Pfam; PF00023; ank; 1.

DR PROSITE; PS50297; ANK\_REP\_REGION; 1.

FT NON\_TER

SQ SEQUENCE 106 AA; 11314 MW; 2D59442F956B6A61 CRC64;

Query Match 67.9%; Score 106; DB 4; Length 106;  
Best Local Similarity 100.0%; Pred. No. 4.7e-92;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	51	VMMGSRVAEELLLHGAEPNCADPATLTPVHDAAREGFLDTLVVLRHAGARLDVRDAM	110
Db	1	VMMGSRVAEELLLHGAEPNCADPATLTPVHDAAREGFLDTLVVLRHAGARLDVRDAM	50
QY	111	GRLPVDLAEELGHRDVARYLRAAAGTGTSNHNARIDAAEGPSDIPD	156
Db	61	GRLPVDLAEELGHRDVARYLRAAAGTGTSNHNARIDAAEGPSDIPD	106

```
RESULT 2
Q9GMF2 PRELIMINARY; PRT; 81 AA.
AC Q9GMF2;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE P16/CDKN2A/MTS1 (FRAGMENT).
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Venkatraj V.S., Mayor J., Modiano J.F.;
RT "Role of p16/Ink4-a in familial canine cancers.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF234176; AAG01087.1; -.
KW Kinase.
SQ SEQUENCE 81 AA; 8868 MW; 0E39D8D805BEAC0F CRC64;
NON_TER 1 1
NON_TER 81 81
Query Match 34.6%; Score 54; DB 6; Length 81;
Best Local Similarity 100.0%; Pred. No. 3.1e-43;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 77 TLRPVDHAAAREGFDTLVVHLHAGARLDVDAWGRLPVDLAEEELGHRDVARYL 130
Db 27 TLRPVDHAAAREGFDTLVVHLHAGARLDVDAWGRLPVDLAEEELGHRDVARYL 80

RESULT 3
Q9XS52 PRELIMINARY; PRT; 86 AA.
AC Q9XS52;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE P15/MTS2/CDKN2B (FRAGMENT).
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Okuda M., Cho K., Setoguchi A., Minehata K., Yazawa M., Endo Y.,
RT Nishigaki K., Watari T., Tsujimoto H., Hasegawa A.;
RL "Cloning and chromosomal mapping of the feline genes p16(MTS1/CDKN2A)
and p15(MTS2/CDKN2B).";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB010808; BAA33541.1; -.
DR HSSP; P55273; 1BD8.
DR InterPro; IPR002110; -.
DR Pfam; PF00023; ank; 2.
DR PROSITE; PS50297; ANK_REP_REGION; 1.
FT NON_TER 1 1
SQ SEQUENCE 86 AA; 9340 MW; A59FF0193290E867 CRC64;
NON_TER 1 1
Query Match 32.7%; Score 51; DB 6; Length 86;
Best Local Similarity 100.0%; Pred. No. 2.2e-40;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 70 PNCADPATLTPRVHDAAREGFDTLVVHLHAGARLDVDAWGRLPVDLAEE 120
Db 20 PNCADPATLTPRVHDAAREGFDTLVVHLHAGARLDVDAWGRLPVDLAEE 70

RESULT 4
Q9XS51 PRELIMINARY; PRT; 102 AA.
AC Q9XS51;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE P16/CDKN2A/MTS1 (FRAGMENT).
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Okuda M., Cho K., Setoguchi A., Minehata K., Yazawa M., Endo Y.,
RT Nishigaki K., Watari T., Tsujimoto H., Hasegawa A.;
RL "Cloning and chromosomal mapping of the feline genes p16(MTS1/CDKN2A)
and p15(MTS2/CDKN2B).";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB010807; BAA33540.1; -.
DR HSSP; P42771; 1B17.
DR InterPro; IPR002110; -.
DR Pfam; PF00023; ank; 3.
DR PROSITE; PS50297; ANK_REP_REGION; 1.
FT NON_TER 1 1
SQ SEQUENCE 102 AA; 10824 MW; 26399FF21359F35D CRC64;
NON_TER 102 102
Query Match 32.7%; Score 51; DB 6; Length 102;
Best Local Similarity 100.0%; Pred. No. 2.5e-40;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 70 PNCADPATLTPRVHDAAREGFDTLVVHLHAGARLDVDAWGRLPVDLAEE 120
Db 20 PNCADPATLTPRVHDAAREGFDTLVVHLHAGARLDVDAWGRLPVDLAEE 70

RESULT 5
Q54846 PRELIMINARY; PRT; 86 AA.
AC Q54846;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE CYCLIN-DEPENDENT KINASE INHIBITOR P15INK4B (FRAGMENT).
GN CDKN2B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Malumbres M., Pellicer A.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF015460; AAB94534.1; -.
DR HSSP; P55273; 1BD8.
DR InterPro; IPR002110; -.
DR PROSITE; PS50297; ANK_REP_REGION; 1.
FT NON_TER 1 1
SQ SEQUENCE 86 AA; 9237 MW; 0499DB26144FB6DF CRC64;
NON_TER 1 1
Query Match 30.8%; Score 48; DB 11; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.5e-37;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 59 VAEILLHGAEPNCADPATLTPRVHDAAREGFDTLVVHLHAGARLDV 106
Db 9 VAEILLHGAEPNCADPATLTPRVHDAAREGFDTLVVHLHAGARLDV 56

RESULT 6
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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 31, 2001, 07:06:13 ; Search time 19.51 Seconds  
(without alignments)  
484.743 Million cell updates/sec

Title: US-09-016-869A-2  
Perfect score: 156  
Sequence: 1 MDPAGSMPEPSDWLATAA.....TRGSNHARIDAAEGPSDIPD 156

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0  
Searched: 412676 seqs, 60623988 residues

Hit size : 0  
Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A\_Geneseq\_0601.\*  
1: /SIDS8/gcgdata/geneseq/geneseq/AA1980.DAT:\*  
2: /SIDS8/gcgdata/geneseq/geneseq/AA1981.DAT:\*  
3: /SIDS8/gcgdata/geneseq/geneseq/AA1982.DAT:\*  
4: /SIDS8/gcgdata/geneseq/geneseq/AA1983.DAT:\*  
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6: /SIDS8/gcgdata/geneseq/geneseq/AA1985.DAT:\*  
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16: /SIDS8/gcgdata/geneseq/geneseq/AA1995.DAT:\*  
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22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	156	100.0	156	16 AAR85116	Cell-cycle regulat
2	156	100.0	156	20 AAY24741	Human INK-4 protei
3	156	100.0	156	21 AAY88354	Human cell cycle r
4	153	98.1	391	18 AAW23534	CDK inhibitory fus
5	153	98.1	391	20 AAW95094	Human p27-p16 fusi
6	153	98.1	391	21 AAY97526	Human W3 protein s
7	153	98.1	391	21 AAY96041	Antiproliferative
8	153	98.1	391	21 AAY96068	Angiogenesis inhib
9	148	94.9	148	16 AAR81701	Multiple tumour su
10	148	94.9	148	16 AAR80940	Human multiple tum
11	148	94.9	151	15 AAR53401	Inhibitor of cycli

12	121	77.6	156	18	AAW10627	Tumour suppressor
13	121	77.6	156	18	AAW19251	Human multiple tum
14	121	77.6	156	19	AAW74549	Amino acid sequenc
15	121	77.6	156	19	AAW40524	Human MTS1 protein
16	121	77.6	156	20	AAW80524	A human multiple t
17	121	77.6	156	21	AAW15498	Human MTS1 protein
18	121	77.6	156	21	AAW97524	Human p16 protein
19	121	77.6	156	21	AAW96053	Human cyclin depen
20	121	77.6	156	21	AAW96067	Human cyclin depen
21	121	77.6	156	21	AAW92921	Human multiple tum
22	121	77.6	156	21	AAW91102	Human multiple tum
23	121	77.6	156	21	AAW59415	Human MTS1 protein
24	121	77.6	156	21	AAW54902	Human multiple tum
25	121	77.6	156	22	AAW67334	Protein encoded by
26	121	77.6	156	22	AAW67390	Human Multiple Tum
27	121	77.6	228	21	AAW97522	Human W9 protein s
28	121	77.6	228	21	AAW96051	Antiproliferative
29	121	77.6	228	21	AAW96078	Angiogenesis inhib
30	121	77.6	237	20	AAW95105	Truncated p27/p16
31	121	77.6	237	21	AAW97534	Human W9 protein s
32	121	77.6	237	21	AAW96049	Antiproliferative
33	121	77.6	237	21	AAW96076	Angiogenesis inhib
34	121	77.6	252	20	AAW95106	Truncated p27/p16
35	121	77.6	252	21	AAW97535	Human W10 protein
36	121	77.6	252	21	AAW96050	Antiproliferative
37	121	77.6	252	21	AAW96077	Angiogenesis inhib
38	121	77.6	323	21	AAW96079	Secretable angio
39	121	77.6	334	20	AAW95103	Truncated p27/p16
40	121	77.6	334	21	AAW97532	Human W8 protein s
41	121	77.6	334	21	AAW96047	Antiproliferative
42	121	77.6	334	21	AAW96074	Angiogenesis inhib
43	121	77.6	365	18	AAW23536	CDK inhibitory fus
44	121	77.6	365	20	AAW95107	Human p16p27 fusio
45	121	77.6	365	20	AAW95096	Human p16p27 fusio

ALIGNMENTS

RESULT 1  
AAR85116  
ID AAR85116 standard; Protein: 156 AA.  
XX AAR85116;  
AC AAR85116;  
XX 01-MAR-1996 (first entry)  
XX Cell-cycle regulatory protein p16.  
XX Cell-cycle regulatory protein p16;  
XX CCR; cancer; cell proliferation.  
XX Homo sapiens.  
XX WO9528483-A1.  
XX 26-OCT-1995.  
XX 14-APR-1995; 95WO-US04636.  
XX 29-NOV-1994; 94US-0346147.  
XX 14-APR-1994; 94US-0227371.  
XX 25-MAY-1994; 94US-0248812.  
XX 14-SEP-1994; 94US-0306511.  
XX (COLD-) COLD SPRING HARBOR LAB.  
XX Beach DH, Demetrick DJ, Hannon GJ, Serrano M;  
XX WPI; 1995-373798/48.  
XX N-PSDB; AAT02962.  
XX New cell cycle regulating proteins bind to cyclin dependent kinase -

PT and related nucleic acids, antibodies etc., used in diagnosis and  
PT therapy of abnormal cell proliferation, degeneration etc.  
XX  
XX  
XX Claim 1; Page 76-77; 109pp; English.  
XX  
XX The human cell-cycle regulatory (CCR) protein p16 (AAR85116) was  
CC obtd. by expression of a cDNA clone (AAT02962) isolated in a 2-hybrid  
CC screening assay. CCR p16 specifically inhibits the activity of  
CC cyclin-dependent kinases during various stages of the cell cycle,  
CC and can be used in the treatment and diagnosis of proliferative  
CC disorders.  
XX  
XX  
SQ Sequence 156 AA;  
  
Query Match 100.0%; Score 156; DB 16; Length 156;  
Best Local Similarity 100.0%; Pred. No. 1.2e-141;  
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
1 MDPAGSSMEPSADWLATAAARGVEEVRALEVALPNAPNSYGRRPQVMMGSAARVA 60  
Db 1 mdpagssmepsadwlataaargveevrallleavalpnapsygrripqvmmggsarva 60  
  
61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAE 120  
Qy 61 ellllhgaepncadpatltrpvhdaaregfdltlvvlrharagldvdrdagrldpvdlaee 120  
Db 61 ellllhgaepncadpatltrpvhdaaregfdltlvvlrharagldvdrdagrldpvdlaee 120  
  
121 LGHRDVARYLRAAGGTRGSHARIDAAGPSDIPD 156  
Qy 121 lghrdvarylraaaggtrgsharidaaegpsdipd 156  
Db 121 lghrdvarylraaaggtrgsharidaaegpsdipd 156  
  
-RESULT 2  
AAV24741  
ID AAY24741 standard; Protein; 156 AA.  
XX  
XX AAY24741;  
XX  
XX 23-AUG-1999 (first entry)  
XX  
XX Human INK-4 protein p16.  
XX  
XX INK-4; p16; p18; p19; CDK4; cell cycle regulatory protein;  
KW transgenic mouse; p16-INK4-a; carcinogen; anti-proliferative.  
XX  
XX Homo sapiens.  
XX  
XX US5919997-A.  
XX  
XX 06-JUL-1999.  
XX  
XX 04-APR-1996; 96US-0627610.  
XX  
XX 04-APR-1996; 96US-0627610.  
XX  
XX 18-NOV-1993; 93US-0154915.  
XX  
XX 14-APR-1994; 94US-0227371.  
XX  
XX 25-MAY-1994; 94US-0248812.  
XX  
XX 14-SEP-1994; 94US-0306511.  
XX  
XX 29-NOV-1994; 94US-0346147.  
XX  
XX 30-JUN-1995; 95US-0497214.  
XX  
XX 02-JAN-1996; 96US-0581918.  
XX  
XX (COLD-) COLD SPRING HARBOR LAB.  
XX  
XX (YESH ) UNIV YESHIVA EINSTEIN COLLEGE.  
XX  
XX Beach DH, DePinho RA, Serrano M;  
XX  
XX WPI; 1999-394656/33.  
XX  
XX N-PSDB; AAX80472.  
XX  
XX Transgenic mice with modified cell-cycle regulation  
XX  
XX Disclosure; Column 45-46; 35pp; English.

XX The present invention describes a transgenic mouse having germline and  
CC somatic cells which comprise an incorporated transgene that disrupts and  
CC inhibits the p16-INK4-a gene leading to tumour susceptibility. Also  
CC described is a method of making a mouse and mouse embryonic stem cells a  
CC functionally disrupted p16-INK4-a gene which comprises transferring a  
CC transgene construct into a mouse embryonic stem cells of a mouse and  
CC transferring these into a mouse blastocyst and implanting the resulting  
CC chimeric blastocyst into a female mouse selecting offspring having an  
CC endogenous p16-INK4-a gene allele. The transgenic mouse is useful for  
CC evaluating the carcinogenic potential or the anti-proliferative activity  
CC of a test compound. The present sequence represents the human INK4  
CC protein p16 given in the present invention.  
XX  
XX  
SQ Sequence 156 AA;  
  
Query Match 100.0%; Score 156; DB 20; Length 156;  
Best Local Similarity 100.0%; Pred. No. 1.2e-141;  
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
1 MDPAGSSMEPSADWLATAAARGVEEVRALEVALPNAPNSYGRRPQVMMGSAARVA 60  
Qy 1 mdpagssmepsadwlataaargveevrallleavalpnapsygrripqvmmggsarva 60  
Db 1 mdpagssmepsadwlataaargveevrallleavalpnapsygrripqvmmggsarva 60  
  
61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAE 120  
Qy 61 ellllhgaepncadpatltrpvhdaaregfdltlvvlrharagldvdrdagrldpvdlaee 120  
Db 61 ellllhgaepncadpatltrpvhdaaregfdltlvvlrharagldvdrdagrldpvdlaee 120  
  
121 LGHRDVARYLRAAGGTRGSHARIDAAGPSDIPD 156  
Qy 121 lghrdvarylraaaggtrgsharidaaegpsdipd 156  
Db 121 lghrdvarylraaaggtrgsharidaaegpsdipd 156  
  
RESULT 3  
AAV88354  
ID AAY88354 standard; Protein; 156 AA.  
XX  
XX AAY88354;  
XX  
XX 14-JUL-2000 (first entry)  
XX  
XX Human cell cycle regulatory protein p16 amino acid sequence.  
XX  
XX Cell cycle regulatory protein; CCR; p16; diagnostic assay; detection;  
KW cell proliferation; differentiation; neoplasia; cancer; cell growth;  
KW cyclin-dependent kinase inhibitor; CDK; human; chromosome 9p21-22.  
XX  
XX Homo sapiens.  
XX  
XX US6043030-A.  
XX  
XX 28-MAR-2000.  
XX  
XX 02-JAN-1996; 96US-0581918.  
XX  
XX 17-DEC-1992; 92US-0991997.  
XX  
XX 18-NOV-1993; 93US-0154915.  
XX  
XX 14-APR-1994; 94US-0227371.  
XX  
XX 25-MAY-1994; 94US-0248812.  
XX  
XX 14-SEP-1994; 94US-0306511.  
XX  
XX 29-NOV-1994; 94US-0346147.  
XX  
XX 30-JUN-1995; 95US-0497214.  
XX  
XX (COLD-) COLD SPRING HARBOR LAB.  
XX  
XX Beach DH, Demetrick DJ, Serrano M, Hannon GJ;  
XX  
XX WPI; 2000-270336/23.  
XX  
XX N-PSDB; AAA13096.  
XX  
XX Use of a mammalian cell cycle regulatory protein (a CDK-inhibitory  
PT protein) in a diagnostic assay for identifying a cell at risk for a

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 31, 2001, 07:02:33 ; Search time 70.99 seconds  
(without alignments)  
167.393 Million cell updates/sec

Title: US-09-016-869A-2  
Perfect score: 800  
Sequence: 1 MDPAGSSMEPSADWLATAA.....TRGSNHARIDAAEGPSDIPD 156  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues  
number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_58:\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	789	98.6	156	2 JE0141	cyclin dependent k
2	529	66.1	130	2 I78845	p15INK4b - mouse
3	526	65.8	138	2 B55479	CDK4 inhibitor p14
4	461.5	57.7	167	2 I58352	p16INK4a - mouse
5	358	32.2	164	2 A57378	cyclin-dependent k
6	249	31.1	166	2 A57379	CDK4/CDK6 inhibito
7	244	30.5	166	2 B57378	cyclin-dependent k
8	231.5	28.9	168	2 B57379	CDK4/CDK6 inhibito
9	228.5	28.6	168	2 A55479	CDK6 inhibitor p18
10	209	26.1	41	2 I52720	gene p15INK4B prot
11	158	19.8	3924	2 S37431	ankyrin 2, neurona
12	137.5	17.2	1848	2 S37771	ankyrin, erythrocy
13	137.5	17.2	1862	2 I49502	ankyrin - mouse
14	133.5	16.7	1856	2 B35049	ankyrin 1, erythro
15	133.5	16.7	1880	2 A35049	ankyrin 1, erythro
16	133.5	16.7	1881	1 SJTHUK	ankyrin 1, erythro
17	131	16.4	857	2 B26294	potassium channel
18	130.5	16.3	1423	1 I37275	death-associated p
19	130	16.2	838	2 S23606	potassium channel
20	130	16.2	1765	2 T42714	ankyrin 3, splice
21	130	16.2	1940	2 T42715	ankyrin 3, splice
22	130	16.2	1943	2 T42713	ankyrin 3, splice
23	130	16.2	1961	2 T42716	ankyrin 3, splice
24	128	16.0	4377	2 A55575	ankyrin 3, long sp
25	127.5	15.9	1786	2 A57282	ankyrin-related pr
26	127.5	15.9	1815	2 T15346	elegans ankyrin-re
27	127.5	15.9	1867	2 T15344	ankyrin-related un
28	127.5	15.9	2039	2 T15347	ankyrin-related un
29	126	15.8	247	2 D84448	probable ankyrin [

30 125 15.6 1964 2 T09059 notch4 - mouse  
31 124.5 15.6 209 2 T5888 hypothetical prote  
32 121 15.1 237 2 T50984 related to 26s pro  
33 121 15.1 888 2 D84650 probable potassium  
34 120 15.0 476 2 T23213 hypothetical prote  
35 118.5 14.8 347 2 C40858 GA-binding protein  
36 118.5 14.8 382 2 B40858 GA-binding protein  
37 117.5 14.7 347 2 C48146 nuclear respirator  
38 117.5 14.7 348 2 I38744 nuclear respirator  
39 117.5 14.7 360 2 I38743 nuclear respirator  
40 117.5 14.7 395 2 I38741 nuclear respirator  
41 117 14.6 1435 2 T32930 hypothetical prote  
42 116.5 14.6 1031 2 T43458 hypothetical prote  
43 116 14.5 1549 2 T13940 ankyrin - fruit fl  
44 115.5 14.4 1058 2 D82654 ankyrin-like prote  
45 114 14.2 828 2 T52046 potassium channel

## ALIGNMENTS

## RESULT 1

JE0141  
cyclin dependent kinase inhibitor - human  
N:Alternate names: CDK4 inhibitor p16(INK4A/MTS1); cyclin-dependent kinase inhibitor  
C:Species: Homo sapiens (man)  
C>Date: 02-Jun-1998 #sequence.revision 10-Jul-1998 #text\_change 19-May-2000  
C:Accession: JE0141; I59268; S39359; I59585; JC5679  
R:Huang, C.G.; Deng, W.; Fu, J.L.  
Chin, J. Biotechnol. 13, 105-107, 1997  
A:Title: Molecular cloning and sequencing of p16 ink4 cDNA from hela cell.  
A:Reference number: JE0141  
A:Accession: JE0141  
A:Molecule type: mRNA  
A:Residues: 1-156 <HUA>  
A:Experimental source: Hella cell  
R:Okamoto, A.; Demetrick, D.J.; Spillare, E.A.; Hagiwara, K.; Hussain, S.P.; Bennett, Proc. Natl. Acad. Sci. U.S.A. 91, 11045-11049, 1994  
A:Note: the sequence is revised in GenBank entry HUMINK4X, release 113.0, PIDN:AAA925  
A:Title: Mutations and altered expression of p16INK4 in human cancer.  
A:Reference number: I59268; MUID:95062202  
A:Accession: I59268  
A>Status: translation not shown; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-152 <OKA>  
A:Cross-references: GB:L27211; NID:g558656; PIDN:AAA92554.1; PID:g558657  
A:Note: the sequence is revised in GenBank entry HUMINK4X, release 113.0, PIDN:AAA925  
R:Serrano, M.; Hannon, G.J.; Beach, D.  
Nature 366, 704-707, 1993  
A:Title: A new regulatory motif in cell-cycle control causing specific inhibition of  
A:Reference number: S39359; MUID:94081956  
A:Accession: S39359  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 9-34, 'V', 36-156 <SEB>  
A:Note: this sequence is corrected in reference I59268  
R:Kamb, A.; Grusis, N.A.; Weaver-Feldhaus, J.; Liu, Q.; Harshman, K.; Tavtigian, S.V.; Science 264, 436-440, 1994  
A:Title: A cell cycle regulator potentially involved in genesis of many tumor types.  
A:Reference number: I59585; MUID:94204645  
A:Accession: I59585  
A>Status: translation not shown; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 51-152 <KAM>  
A:Cross-references: GB:S69804; NID:g546272; PIDN:AAAD14048.1; PID:g4261748  
C:Comment: This protein inhibits the activity of cyclin D1/CDK4 and cyclin D1/CDK6 k1  
C:Genetics:  
A:Gene: GDB:CDKN2A; CDK4I; MLM; P16; INK4; MTS1; CMM2; CDKN2  
A:Cross-references: GDB:335362; OMIM:600160  
A:Map position: 9p21-9p21  
C:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homol  
C:Keywords: cell cycle control; protein kinase inhibitor; tumor suppressor

```
Query Match      57.7%   Score 461.5; DB 2; Length 167;
Best Local Similarity 53.2%; Pred. No. 4.7e-36;
Matches 98; Conservative 16; Mismatches 32; Indels 9; Gaps 3;
```

69	QY	EFNCADPATLTRPVHDAAREGFLDTLVLHHRAGARLVDYRDAGWLPLVDLAELGLGHDVAR	128
60	Db	DSNCEDPDTTFSPVHDAAREGFLDTLVLHGHSGARLVDYRDAGWLPLDLAQRGHQDIVR	119
129	QY	YLRAA-----AGCT--RGSNHARIDAAEGPSDIP	155
120	Db	YLRSAGCSLCSAGWSLCTAGNVAOTDGHFSFSSTP	154

RESULT 5

A57378

cyclin-dependent kinase inhibitor p19 - human

C:Species: Homo sapiens (man)

C:Date: 08-Feb-1996 #sequence\_revision 08-Feb-1996 #text\_change 22-Jun-1999

C:Accession: A57378

R:Chan, F.K.M.; Zhang, J.; Cheng, L.; Shapiro, D.N.; Winoto, A.  
Mol. Cell. Biol. 15, 2682-2688, 1995

A:Title: Identification of human and mouse p19, a novel CDK4 and CDK6 inhibitor

A:Reference number: A57378; MUID:95257949

A:Accession: A57378

A:Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-164 <CHA>

A:Cross-references: GB:U20498

C:Genetics:

C:Superfamily: unassigned ankryrin repeat proteins; ankryrin repeat homology;

C:Map position: 19p13

```
Query Match      32.2%; Score 258; DB 2; Length 164;
Best Local Similarity 44.1%; Pred. No. 4.8e-17;
Matches 67; Conservative 17; Mismatches 62; Indels 6; Gaps 3;
```

---

```
QY    10 EP$ADWLATAAARGVEEV$RALL--ENAVLPNAPNSYGRERFIOVMMG$ARVAELLILLHCA 68
       ||| :|||||::||| ||| :||| :||| :||| :||| :||| :||| :||| :|||
Db     5 EVRAGTLSGAARGVDQEV$RLLHRELVHPDALARFGKTAQLQVMPFG$TAIALELLKOGA 64
       ||| :|||||::||| ||| :||| :||| :||| :||| :||| :||| :||| :|||
QY    69 EPNCADPATLTPRVHDAAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEEELGH$RDVAR 128
       ||| :|||||::||| ||| :||| :||| :||| :||| :||| :||| :||| :|||
Db     65 SPNVQDTSG-TSPVHDAARTGFELDTKLVLVEHGADVNPVGTCALPIHLAVOEGHTAVVS 123
       ||| :|||||::||| ||| :||| :||| :||| :||| :||| :||| :||| :|||
QY    129 YLR$AAG----GTRGSNHARIDAAEGPSDIPD 156
       ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db    124 FLAASDLHRRDARGITPLEALORGADIVD 155
       ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
```

RESULT 6

A57379

C:CDK6 inhibitor p19 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 08-Feb-1996 #sequence\_revision 08-Feb-1996 #text\_change 20-Sep-1999

C:Accession: A57379

R:Hirai, H.; Roussel, M.F.; Kato, J.Y.; Ashmun, R.A.; Sherr, C.J. Mol. Cell. Biol. 15, 2672-2681, 1995

A:Title: Novel INK4 proteins, p19 and p18, are specific inhibitors of the cyclin D-dependent kinase p34<sup>cdc2</sup>

A:Reference number: A57379; MUID:95257948

A:Accession: A57379

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-166 <HRR>

A:Cross-references: GB:U19597; NID:g790568; PID:AAC52194.1; PID:g790569

C:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology

C:Keywords: cell cycle control

EGF homology

```

Query Match      31.1%  Score 249;  DB 2;  Length 166;
Best Local Similarity 44.3%;  Pred. No. 3.4e-16;
Matches         70;  Conservative 18;  Mismatches 52;  Indels 18;  Gaps 5;

Qy  14  DLWLATAAARGVEEVRAL-EEAVALPNAPSYGRRPQIVVMGMSARVAEILLIHGAEPNC 72
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db  10  DRLSGARARGDVOEVRLLHRELVPDALNFGKLTQVMVFGPSAVALLELKGASPNV 69
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

Qy	73	ADP	ATLTP	PPV	HDAA	BE	GF	LT	VL	VH	HR	AG	AR	LD	VR	DG	NR	GL	PD	LA	EE	LG	HR	DA	RY	--	130	
Db	70	QD	-	AS	GF	SE	VD	HA	AR	TG	LT	LT	KL	VL	VE	HD	AG	NA	LD	TG	SL	PI	HL	AT	RE	GH	SV	128
Qy	131	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	155	
Db	129	ES	DL	HR	DA	SG	LT	PLE	LA	OR	GA	NI	-	MD	T	LO	G	H	M	M	P	-	-	-	-	-	-	165

```

RESULT      7
B57378
cyclin-dependent kinase inhibitor p19 - mouse
C:Species: Mus musculus (house mouse)
C:date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 20-Sep-1999
C:Accession: B57378
A:Chan, F.K.M.; Zhang, J.; Cheng, L.; Shapiro, D.N.; Winoto, A.
Mol. Cell. Biol. 15, 2682-2688, 1995
A:title: Identification of human and mouse p19, a novel CDK4 and CDK6 inhibitor with
A:Reference number: A57378; MUID:95257949
A:Accession: B57378
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-166 <CHA>
A:Cross-references: GB:U020497; NID:g91204; PIDN:AAA85437.1; PID:g791205
C:Superfamily: unassigned ankryrin repeat proteins; ankryrin repeat homology; EGF homology;

```

```

Query Match          30.5%; Score 244; DB 2; Length 166;
Best Local Similarity 43.7%; Pred. No. 9,8e-153;
Matches 69; Conservative 18; Mismatches 56; Indels 18; Gaps 5;

QY      14 DWLATAAAAGRYEEVRALL-FAVALPNAPNSYGRRPLOVMMGSGSAVLELLHLHGAEPNC 72
      | | : | | | | | | | : | | : | | | | | | | | | | | | | | | |
Db       10 DRUGSARPGDVOEYRLLHRELVHPDNLNFGKLTALQVMFGSPAVALLELLKQGSAPNV 69
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      73 ADPATITRPVHDAAREGFDTLVLHRAGARLDVYRDAGRLPDLAELGHRDVRYL-- 130
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       70 QD-ASGTSVPHDAARTGFDTLKVLVEHGADVNALDTSGLPILHAI REGHSVVSFLAP 128
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY      131 -----RAAAGCT-----RGSNHARIDAAEGSPDIP 155
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db       129 ESDLHHRDASGLTPTLELARAQCAONL-MDILQGHMMP 165
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

```

RESULT      8
B57379
CDK4/CDK6 inhibitor p18 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 08-Feb-1996 #sequence_revision
C:Accession: B57379
R:Hirai, H.; Roussel, M.F.; Kato, J.Y.; Ashmun, R.A.; Sherr, C.J.
Mol. Cell. Biol. 15, 2672-2681, 1995
A:Title: Novel INK4 proteins, p19 and p18, are specific inhibitors of the cyclin D-de
A:Reference number: A57379; MUID:95257948
A:Accession: B57379
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-168 <HR>
A:Cross-references: GB:U19596; NID:g790566; PID:AAC52193.1; PID:g790567
C:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homol
C:Keywords: cell cycle control

```

[illegible]

Db 63 PNLKD-GTGFVHDAARAGFLDTVOALLERQADVNIEDNEGNLPLHLAAKEGHLPVVEF 121

QY 130 LRAAAGGTGRGSHARIDAA 148

Db 122 LMKHTACNVGHRNHKGDTA 140

RESULT 9

ANK6 inhibitor p18 - human

N:Alternate names: cyclin-dependent kinase inhibitor 2C; D-type cyclin-dependent kinase

C:Species: Homo sapiens (man)

C:Date: 23-Mar-1995 #sequence\_revision 23-Mar-1995 #text\_change 20-Sep-1999

C:Accession: A55479

R:Chan, W.

A:Reference number: A55479

A:Title: Isolation and characterization of cDNAs encoding human brain ankyrins reveal

A:Reference number: A55479

A:Accession: A55479

A:Molecule type: mRNA

A:Residues: 1-168 <GUA>

A:Cross-references: GB:U17074; NID:g639713; PIDN:AA50074.1; PID:g639714

C:Genetics:

A:Gene: GDB:CDKN2C

A:Cross-references: GDB:594931

A:Map position: 1p32-1p32

A:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology

C:Keywords: cell cycle control; protein kinase inhibitor; tumor suppressor

Query Match 28.6%; Score 228.5; DB 2; Length 168;

Best Local Similarity 40.3%; Pred. No. 2.8e-14;

Matches 56; Conservative 22; Mismatches 60; Indels 1; Gaps 1;

QY 10 EPSADWLATAAAGRVEEVALLEVALPNAPNSYGRRIQVMMGSAARVAELLLHGA 69

Db 3 EPWGNELASAAARGDLQLTSLQNNVNVNAQNGFGRTALQVNMKGNPETARRLLLRGAN 62

QY 70 PNCADPATLTPRHDAAREGFLDTVLVHRAGARLDVDAWGLPVDLAELGHRDVARY 129

Db 63 PDLKD-RTGFVHDAARAGFLDTLTLEFFQADVNIEDNEGNLPLHLAAKEGHLRVVEF 121

QY 130 LRAAAGGTGRGSHARIDAA 148

Db 122 LVKHTASNVGHRNHKGDTA 140

RESULT 10

p15INK4B protein - rat (fragment)

C:Species: Rattus sp. (rat)

C:Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 26-May-2000

C:Accession: I52720

R:Knapek, D.F.; Serrano, M.; Beach, D.; Trono, D.; Walker, C.L.

Cancer Res. 55, 1607-1612, 1995

A:Title: Association of rat p15INK4B/p16INK4 deletions with monosomy 5 in kidney epithel

A:Reference number: I52720; MUID:95228036

A:Accession: I52720

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-41 <RES>

A:Cross-references: GB:S77734; NID:g998711

C:Genetics:

A:Gene: p15INK4B

C:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology

Query Match 26.1%; Score 209; DB 2; Length 41;

Best Local Similarity 97.6%; Pred. No. 3.8e-13;

Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 52 MMGSAQVAELLLLHGAPNCADPATLTPRVHDAAREGFLD 92

Db 1 MMGSAQVAELLLLHGAPNCADPATLTPRVHDAAREGFLD 41

RESULT 11

ankyrin 2, neuronal long splice form - human

N:Alternate names: ankyrin B, 440K splice form; ankyrin-B; brain ankyrin; non-erythro

N:Contains: ankyrin 2, short form

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 13-Aug-1999

C:Accession: S37431; A39643; B39643; A40334; A49462; S14533; S14569

R:Chan, W.

A:Reference number: S37431

A:Accession: S37431

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-3924 <CHA>

A:Cross-references: EMBL:Z26634; NID:g406287; PIDN:CAA81387.1; PID:g406288

R:Otto, E.; Kunimoto, M.; McLaughlin, T.; Bennett, V.

J. Cell Biol. 114, 241-253, 1991

A:Title: Isolation and characterization of cDNAs encoding human brain ankyrins reveal

A:Reference number: A39643; MUID:91302466

A:Accession: A39643

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-2077 <OTL>

A:Cross-references: GB:X56957

A:Accession: B39643

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 463-474, 'PE', 477-495 <TSE>

A:Cross-references: GB:M37123; NID:gl78647; PIDN:AAA62828.1; PID:gl78648

R:Chan, W.; Kordeli, E.; Bennett, V.

J. Cell Biol. 123, 1463-1473, 1993

A:Title: 440-kD ankyrinB: structure of the major developmentally regulated domain and

A:Reference number: A49462; MUID:94075409

A:Accession: A49462

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-3924 <RES>

A:Cross-references: EMBL:Z26634; NID:g406287; PIDN:CAA81387.1; PID:g406288

C:Genetics:

A:Gene: GDB:ANK2

A:Cross-references: GDB:127607; OMIM:106410

A:Map position: 4q25-4q27

C:Superfamily: ankyrin; ankyrin repeat homology

C:Keywords: alternative splicing

F:2-3924/Product: ankyrin 2, long form #status predicted <MA>

F:2-1443.3585-3924/Product: ankyrin 2, short form #status predicted <MA2>

F:63-95/Domain: ankyrin repeat homology <AN01>

F:96-128/Domain: ankyrin repeat homology <AN02>

F:129-161/Domain: ankyrin repeat homology <AN03>

F:162-190/Domain: ankyrin repeat homology <AN04>

F:191-223/Domain: ankyrin repeat homology <AN05>

F:232-264/Domain: ankyrin repeat homology <AN06>

F:265-297/Domain: ankyrin repeat homology <AN07>

F:298-330/Domain: ankyrin repeat homology <AN08>

F:331-363/Domain: ankyrin repeat homology <AN09>

F:364-396/Domain: ankyrin repeat homology <AN10>

F:397-429/Domain: ankyrin repeat homology <AN11>

F:430-462/Domain: ankyrin repeat homology <AN12>

F:463-495/Domain: ankyrin repeat homology <AN13>

F:496-528/Domain: ankyrin repeat homology <AN14>

F:529-561/Domain: ankyrin repeat homology <AN15>

Query Match 17.2%; Score 137.5; DB 2; Length 1848;  
Best Local Similarity 34.7%; Pred. NO. 0.00013;  
Matches 51; Conservative 17; Mismatches 68; Indels 11;

## RESULT 14

B35049  
ankyrin 1, erythrocyte splice form 3 - human  
N:Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R  
N:Contains: ankyrin 2.2, erythrocyte  
C:Species: Homo sapiens (man)  
C:Date: 17-Nov-1995 #sequence\_revision 17-Nov-1995 #text\_change 10-Jul-1998  
C:Accession: B35049  
R:Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; K  
Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990  
A:Title: cDNA sequence for human erythrocyte ankyrin.  
A:Reference number: A35049; MUID:90175370

A:Accession: B35049

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1856 <LAW>

C:Genetics:

A:Gene: GDB:ANK1; ANK

A:Cross-references: GDB:118737; OMIM:182900

A:Map position: 8p11.2-8p11.2

C:Superfamily: ankyrin; ankyrin repeat homology

C:Keywords: alternative splicing

F:2-1856/Product: ankyrin 1, erythrocyte form 3 #status predicted <MAT>

F:2-1513,1676-1856/Product: ankyrin 2.2, erythrocyte #status predicted <MA2>

F:44-76/Domain: ankyrin repeat homology <AN01>

F:77-109/Domain: ankyrin repeat homology <AN02>

F:110-142/Domain: ankyrin repeat homology <AN03>

F:143-171/Domain: ankyrin repeat homology <AN04>

F:172-204/Domain: ankyrin repeat homology <AN05>

F:205-237/Domain: ankyrin repeat homology <AN06>

F:238-270/Domain: ankyrin repeat homology <AN07>

F:271-303/Domain: ankyrin repeat homology <AN08>

F:304-336/Domain: ankyrin repeat homology <AN09>

F:337-369/Domain: ankyrin repeat homology <AN10>

F:370-402/Domain: ankyrin repeat homology <AN11>

F:403-435/Domain: ankyrin repeat homology <AN12>

F:436-468/Domain: ankyrin repeat homology <AN13>

F:469-501/Domain: ankyrin repeat homology <AN14>

F:502-534/Domain: ankyrin repeat homology <AN15>

F:535-567/Domain: ankyrin repeat homology <AN16>

F:568-600/Domain: ankyrin repeat homology <AN17>

F:601-633/Domain: ankyrin repeat homology <AN18>

F:634-666/Domain: ankyrin repeat homology <AN19>

F:667-699/Domain: ankyrin repeat homology <AN20>

F:700-732/Domain: ankyrin repeat homology <AN21>

F:733-765/Domain: ankyrin repeat homology <AN22>

F:766-798/Domain: ankyrin repeat homology <AN23>

Query Match 16.7%; Score 133.5; DB 2; Length 1856;

Best Local Similarity 35.4%; Pred. No. 0.00032;

Matches 52; Conservative 15; Mismatches 69; Indels 11; Gaps 6;

Qy 16 LATAAARGVEEVRALLEAVLPNAPNSYGRRTPIQV-MMGSAARVAELLLHGAEPNCAD 74

Db 507 LHIAAREGHVETVLALLEKEASQACMTKGGFTPLHVAAYKGVKRVAEILLERDAHPNAAG 566

Qy 75 PATLTRPVHDAAREGFDLT-L-VVLRAGARLDVRDAW-GRLPVDLAELGHRDVARVYL-- 130

Db 567 KNGLT-PLHVAVHHNNLDIVKLLPRGGS--PHSPAWNGYTPPLHIAAKQNOVEARSLLQ 623

Qy 131 ---RAAAGTGRGSHARIDAEGPSDI 154

Db 624 YGGSANAEVQGVTPPLHAAQEGHAEM 650

## RESULT 15

A35049  
ankyrin 1, erythrocyte splice form 2 - human  
N:Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R  
N:Contains: ankyrin 2.2, erythrocyte  
C:Species: Homo sapiens (man)

C:Date: 27-Jul-1990 #sequence\_revision 01-Oct-1992 #text\_change 04-Sep-1998  
C:Accession: A35049  
R:Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.

Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990

A:Title: cDNA sequence for human erythrocyte ankyrin.

A:Reference number: A35049; MUID:90175370

A:Accession: A35049

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1880 <LAW>

A:Cross-references: GDB:M28880

C:Genetics:

A:Gene: GDB:ANK1; ANK

A:Cross-references: GDB:118737; OMIM:182900

A:Map position: 8p11.2-8p11.2

C:Superfamily: ankyrin; ankyrin repeat homology

C:Keywords: alternative splicing; cytoskeleton

F:2-1880/Product: ankyrin 1, erythrocyte form 2 #status predicted <MAT>

F:2-1513,1676-1880/Product: ankyrin 2.2, erythrocyte #status predicted <MA2>

F:44-76/Domain: ankyrin repeat homology <AN01>

F:77-109/Domain: ankyrin repeat homology <AN02>

F:110-142/Domain: ankyrin repeat homology <AN03>

F:143-171/Domain: ankyrin repeat homology <AN04>

F:172-204/Domain: ankyrin repeat homology <AN05>

F:205-237/Domain: ankyrin repeat homology <AN06>

F:238-270/Domain: ankyrin repeat homology <AN07>

F:271-303/Domain: ankyrin repeat homology <AN08>

F:304-336/Domain: ankyrin repeat homology <AN09>

F:337-369/Domain: ankyrin repeat homology <AN10>

F:370-402/Domain: ankyrin repeat homology <AN11>

F:403-435/Domain: ankyrin repeat homology <AN12>

F:436-468/Domain: ankyrin repeat homology <AN13>

F:469-501/Domain: ankyrin repeat homology <AN14>

F:502-534/Domain: ankyrin repeat homology <AN15>

F:535-567/Domain: ankyrin repeat homology <AN16>

F:568-600/Domain: ankyrin repeat homology <AN17>

F:601-633/Domain: ankyrin repeat homology <AN18>

F:634-666/Domain: ankyrin repeat homology <AN19>

F:667-699/Domain: ankyrin repeat homology <AN20>

F:700-732/Domain: ankyrin repeat homology <AN21>

F:733-765/Domain: ankyrin repeat homology <AN22>

F:766-798/Domain: ankyrin repeat homology <AN23>

Query Match 16.7%; Score 133.5; DB 2; Length 1880;

Best Local Similarity 35.4%; Pred. No. 0.00032;

Matches 52; Conservative 15; Mismatches 69; Indels 11; Gaps 6;

Qy 16 LATAAARGVEEVRALLEAVLPNAPNSYGRRTPIQV-MMGSAARVAELLLHGAEPNCAD 74

Db 507 LHIAAREGHVETVLALLEKEASQACMTKGGFTPLHVAAYKGVKRVAEILLERDAHPNAAG 566

Qy 75 PATLTRPVHDAAREGFDLT-L-VVLRAGARLDVRDAW-GRLPVDLAELGHRDVARVYL-- 130

Db 567 KNGLT-PLHVAVHHNNLDIVKLLPRGGS--PHSPAWNGYTPPLHIAAKQNOVEARSLLQ 623

Qy 131 ---RAAAGTGRGSHARIDAEGPSDI 154

Db 624 YGGSANAEVQGVTPPLHAAQEGHAEM 650

Search completed: October 31, 2001, 07:06:09  
Job time: 216 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 31, 2001, 07:03:43 ; Search time 33.95 Seconds  
(without alignments)  
157.404 Million cell updates/sec

Title: US-09-016-869A-2  
Perfect score: 800  
Sequence: 1 MDPAGSSMEPSADWLATAA.....TRGSNHARIDAAEGPSDIPD 156

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

! number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	789	98.6	156	CDN2_HUMAN	P42771 homo sapien
2	529	66.1	130	CDN5_MOUSE	P55271 mus musculu
3	526	65.8	138	CDN5_HUMAN	P42772 homo sapien
4	524	65.5	130	CDN5_RAT	P55272 rattus norv
5	461.5	57.7	167	CDN2_MOUSE	P51480 mus musculu
6	408	51.0	171	CDN2_MONDO	O77617 monodelphis
7	259	32.4	166	CDN7_HUMAN	P55273 homo sapien
8	249	31.1	166	CDN7_MOUSE	Q60773 mus musculu
9	231.5	28.9	168	CDN6_MOUSE	Q60772 mus musculu
10	228.5	28.6	168	CDN6_HUMAN	P42773 homo sapien
11	158	19.8	3924	ANK2_HUMAN	Q01484 homo sapien
12	137.5	17.2	1862	ANK1_MOUSE	Q02357 mus musculu
13	133.5	16.7	1880	ANK1_HUMAN	P16157 homo sapien
14	130.5	16.3	1431	DAPK_HUMAN	P53355 homo sapien
15	125	15.6	1964	NTC4_MOUSE	P31695 mus musculu
16	118.5	14.8	347	GABG_MOUSE	Q00421 mus musculu
17	118.5	14.8	382	GABG_MOUSE	Q00420 mus musculu
18	117.5	14.7	347	GABG_HUMAN	Q06545 homo sapien
19	117.5	14.7	383	GABG_HUMAN	Q06547 homo sapien
20	114	14.2	768	BARL_RAT	Q9qzh2 rattus norv
21	114	14.2	2437	NOTC_CHRVE	P46530 brachydanio
22	112	14.0	323	ANKH_CHRVI	Q06527 chromidam
23	111.5	13.9	2531	NTC1_RAT	Q07008 rattus norv
24	111	13.9	777	BARL_HUMAN	Q99728 homo sapien
25	110.5	13.8	2444	NTC1_HUMAN	P46531 homo sapien
26	109.5	13.7	832	ANK3_HUMAN	P57078 homo sapien
27	107.5	13.4	2703	NOTC_DROME	P07207 drosophila
28	107	13.4	765	BARL_MOUSE	O70445 mus musculu
29	104.5	13.1	1178	PHB1_YEAST	P17442 saccharomyc
30	104.5	13.1	2524	NOTC_XENLA	P21783 xenopus lae
31	103.5	12.9	740	Y050_HUMAN	Q15027 homo sapien
32	103.5	12.9	2318	NTC3_MOUSE	Q61982 mus musculu
33	103	12.9	679	RN5A_MOUSE	Q05921 mus musculu

ALIGNMENTS

RESULT 1

ID	CDN2_HUMAN	STANDARD;	PRT;	156 AA.
AC	P42771: Q15191;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I) (P16-INK4) (P16-INK4A)			
DE	(MULTIPLE TUMOR SUPPRESSOR 1) (MTS1).			
GN	CDKN2A OR CDKN2.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=94081956; PubMed=8259215;			
RA	Serrano M., Hannon G.J., Beach D.;			
RA	"A new regulatory motif in cell-cycle control causing specific			
RT	inhibition of cyclin D/CDK4.";			
RL	Nature 366:704-707(1993).			
RN	[2]			
RP	SEQUENCE OF 51-152 FROM N.A.			
RX	MEDLINE=94204645; PubMed=8153634;			
RA	Kamb A., Gruis N.A., Weaver-Feidhaus J., Liu Q., Harshman K.,			
RA	Tavtigian S.V., Stockert E., Day R.S. III, Johnson B.E.,			
RA	Skolnick M.H.;			
RT	"A cell cycle regulator potentially involved in genesis of many tumor			
RT	types.";			
RL	Science 264:436-440(1994).			
RN	[3]			
RP	SEQUENCE OF 1-20 FROM N.A.			
RX	MEDLINE=96182088; PubMed=8622687;			
RA	Hara E., Smith R., Parry D., Tahara H., Stone S., Peters G.;			
RA	"Regulation of p16CDKN2 expression and its implications for cell			
RT	immortalization and senescence.";			
RL	Mol. Cell. Biol. 16:859-867(1996).			
RN	[4]			
RP	X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH CDK6.			
RX	MEDLINE=98421670; PubMed=9751050;			
RA	Russo A.A., Tong L., Lee J.O., Jeffrey P.D., Pavletich N.P.;			
RA	"Structural basis for inhibition of the cyclin-dependent kinase Cdk6			
RT	by the tumour suppressor p16INK4a.";			
RL	Nature 395:237-243(1998).			
RN	[5]			
RP	REVIEW ON MELANOMA VARIANTS.			
RX	MEDLINE=96377761; PubMed=8783570;			
RA	Dracopoli N.C., Fountain J.W.;			
RA	"CDKN2 mutations in melanoma.";			
RL	Cancer Surv. 26:115-132(1996).			
RN	[6]			
RP	REVIEW ON VARIANTS.			
RX	MEDLINE=96303699; PubMed=8723678;			
RA	Smith-Soerensen B., Hovig E.;			
RA	"CDKN2A (p16INK4A) somatic and germline mutations.";			
RL	Hum. Mutat. 7:294-303(1996).			

P81069 mus musculu  
Q03017 drosophila  
Q09103 drosophila  
Q19013 caenorhabdi  
P18954 serratia li  
Q14161 homo sapien  
Q00653 homo sapien  
Q01705 mus musculu  
Q60649 mus musculu  
P53356 hydra atten  
Q99490 homo sapien  
Q15057 homo sapien

17] VARIANTS NON-SMALL CELL LUNG CARCINOMAS (NSCLC).  
RN MEDLINE-94338359; PubMed=80609323;  
RX Hayashi N., Sugimoto Y., Tsuchiya E., Ogawa M., Nakamura Y.;  
RA "Somatic mutations of the MTS (multiple tumor suppressor) 1/CDK41  
RT (cyclin-dependent kinase-4 inhibitor) gene in human primary non-small  
RT cell lung carcinomas.";  
RL Biochem. Biophys. Res. Commun. 202:1426-1430(1994).  
[8]  
RN VARIANTS MELANOMA THR-49; PRO-71; TRP-101; ASP-126 & THR-148.  
RX MEDLINE-95078916; PubMed=7987387;  
RA Hussussian C.J., Struwing J.P., Goldstein A.M., Higgins P.A.T.,  
RT Ally D.S., Sheahan M.D., Clark W.H. Jr., Tucker M.A., Dracopoli N.C.;  
RL "Germline p16 mutations in familial melanoma.";  
RN Nat. Genet. 8:15-21(1994).  
[9]  
RN VARIANTS SOUMAMOUS CELL CARCINOMA (SCCA) SER-127 AND CYS-144.  
RX MEDLINE-95060835; PubMed=7970734;  
RA Zhou X., Tarmin L., Yin J., Jiang H.-Y., Suzuki H., Rhyu M.-G.,  
RT Abraham J.M., Melitzer S.J.;  
RL "The MTS1 gene is frequently mutated in primary human esophageal  
tumors.";  
RN Oncogene 9:3737-3741(1994).  
[10]  
RN VARIANTS  
RX MEDLINE-95188190; PubMed=7882351;  
RA Okamoto A., Hussain S.P., Hagiwara K., Spillare E.A., Rusin M.R.,  
RA Bennett W.P., Forrester K., Gerwin B., Beach D.H., Harris C.C.;  
RT "Mutations in the p16INK4/MTS1/CDKN2, p15INK4B/MTS2, and p18 genes in  
primary and metastatic lung cancer.";  
RL Cancer Res. 55:1448-1451(1995).  
[11]  
RN VARIANTS MELANOMA P-32; A-35; E-35; R-50; I-53, AND VARIANT T-148.  
RX MEDLINE-96121580; PubMed=8595405;  
RA Walker G.J., Hussussian C.J., Flores J.F., Glendening J.M.,  
RA Haluska F.G., Dracopoli N.C., Hayward N.K., Fountain J.W.;  
RT "Mutations of the CDKN2/p16INK4 gene in Australian melanoma  
kindreds.";  
RL Hum. Mol. Genet. 4:1845-1852(1995).  
[12]  
RN CHARACTERIZATION OF VAR. T-49; S-71; L-81; P-87; W-101; D-126 & T-148.  
RX MEDLINE-95375774; PubMed=7647780;  
RA Ranade K., Hussussian C.J., Sikorski R.S., Varmus H.E.,  
RA Goldstein A.M., Tucker M.A., Serrano M., Hannon G.J., Beach D.,  
RA Dracopoli N.C.;  
RT "Mutations associated with familial melanoma impair p16INK4  
function.";  
RL Nat. Genet. 10:114-116(1995).  
[13]  
RN VARIANTS MELANOMA I-53 AND C-107, AND VARIANTS V-68; T-85 AND T-148.  
RX MEDLINE-96323259; PubMed=8710906;  
RA Fitzgerald M.G., Harkin D.P., Silva-Arrieta S., Macdonald D.J.,  
RA Lucchina L.C., Unsal H., O'Neill E., Koh J., Finkelstein D.M.,  
RA Isselbacher K.J., Sober A.J., Haber D.A.;  
RT "Prevalence of germ-line mutations in p16, p19ARF, and CDK4 in  
familial melanoma: analysis of a clinic-based population.";  
RL Proc. Natl. Acad. Sci. U.S.A. 93:8541-8545(1996).  
[14]  
RN VARIANTS MELANOMA PRO-24; ILE-53 AND THR-118, AND VARIANT THR-148.  
RX MEDLINE-97472457; PubMed=9328469;  
RA Harland M., Meloni R., Gruis N., Pinney E., Brookes S., Spurr N.K.,  
RA Frischauf A.-M., Bataille V., Peters G., Cuzick J., Selby P.,  
RA Bishop D.T., Bishop J.N.;  
RT "Germline mutations of the CDKN2 gene in UK melanoma families.";  
RL Hum. Mol. Genet. 6:2061-2067(1997).  
[15]  
RN VARIANTS FAMILIAL MELANOMA.  
RX MEDLINE-98087572; PubMed=9425228;  
RA Soufir N., Avril M.-F., Chompret A., Demenais F., Bomblard J.,  
RA Spatz A., Stoppa-Lyonnet D., Benard J., Bressac-De Paillerets B.;  
RT "Prevalence of p16 and CDK4 germline mutations in 48 melanoma-prone  
families in France.";  
RN Hum. Mol. Genet. 7:209-216(1998).  
[16]  
RN ERATUM.  
RA Soufir N., Avril M.-F., Chompret A., Demenais F., Bomblard J.,  
RA Spatz A., Stoppa-Lyonnet D., Benard J., Bressac-De Paillerets B.;  
RN Hum. Mol. Genet. 7:941-941(1998).  
[17]  
RN VARIANT PANCREATIC CARCINOMA CYS-146.  
RA Moskaluk C.A., Hruban R.H., Lietman A., Smyrk T., Fusaro L.,  
RA Fusaro R., Lynch J., Yeo C.J., Jackson C.E., Lynch H.T., Kern S.E.;  
RT "Novel germline p16INK4 allele (Asp145Cys) in a family with multiple  
pancreatic carcinomas.";  
RL Hum. Mutat. 12:70-70(1998).  
[18]  
RN VARIANTS MELANOMA LEU-48; VAL-57; ASP-89 AND MET-117.  
RA Gretsardottir S., Olafsdottir G.H., Borg A.;  
RT glioma and carcinoma of the pancreas.";  
RL Hum. Mutat. 12:212-212(1998).  
CC - FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS ITS  
REGULATOR OF THE PROLIFERATION OF NORMAL CELLS.  
CC ABILITY TO INTERACT WITH CYCLINS D. COULD ACT AS A NEGATIVE  
SUBUNIT: HETERODIMER WITH CDK4 OR CDK6.  
CC - DISEASE: CDKN2A MUTATIONS ARE INVOLVED IN TUMOR FORMATION IN A  
WIDE RANGE OF TISSUES.  
CC - SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE  
INHIBITORS.  
CC - SIMILARITY: CONTAINS 4 ANK REPEATS.  
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CC  
EMBL; L27211; AAA92554.1; -  
DR EMBL; U12820; AAB60645.1; -  
DR EMBL; U12818; AAB60645.1; JOINED.  
DR EMBL; U12819; AAB60645.1; JOINED.  
DR EMBL; S69804; AAD14048.1; -  
DR EMBL; X94154; CAA63870.1; -  
DR PDB; 1BI7; 16-FEB-99.  
DR MIM; 600160; -  
DR InterPro; IPR002110; -  
DR Pfam; PF00023; ank; 3.  
DR PROSITE; PS0297; ANK\_REPEAT\_REGION; 1.  
KW Cell cycle; Anti-oncogene; Repeat; ANK repeat; Disease mutation;  
KW Polymorphism; Li-Fraumeni syndrome; 3D-structure.  
FT REPEAT 11 40 ANK 1.  
FT REPEAT 44 72 ANK 2.  
FT REPEAT 77 106 ANK 3.  
FT REPEAT 110 139 ANK 4.  
FT VARIANT 14 14 D -> E (IN A BILIARY TRACT TUMOR).  
FT VARIANT 16 16 L -> P (IN A BILIARY TRACT TUMOR AND A  
FAMILIAL MELANOMA).  
FT VARIANT 20 20 A -> P (IN A LONG TUMOR AND MELANOMA).  
FT VARIANT 20 20 A -> S (IN A BILIARY TRACT TUMOR).  
FT VARIANT 23 23 G -> D (IN A PANCREAS TUMOR).  
FT VARIANT 24 24 R -> C (IN MELANOMA).  
FT VARIANT 24 24 R -> P (IN FAMILIAL MELANOMA AND  
MELANOMA).  
FT VARIANT 26 26 E -> D (IN A BILIARY TRACT TUMOR).  
FT VARIANT 32 32 L -> P (IN FAMILIAL MELANOMA).

Query Match 98.6%; Score 789; DB 1; Length 156;  
 Best Local Similarity 98.7%; Pred. No. 3.5e-66;  
 Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDPAGSSMEPSADWLTAAAGRVVEEVRALLLEAVLNPAPNSYGRRPITQVMMGSAVA 60  
 Db 1 MEPAAGSSMEPSADWLTAAAGRVVEEVRALLLEAGALNPAPNSYGRRPITQVMMGSAVA 60

QY 61 ELLLLHGAEPCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVDRWAGRLPVDIAEE 120  
 Db 61 ELLLLHGAEPCADPATLTPRVHDAAREGFLDTLVVLRHAGARLDVDRWAGRLPVDIAEE 120

QY 121 LGHROVARYLRAAAGTRGSHARIDAAEGPSDIPD 156  
 Db 121 LGHROVARYLRAAAGTRGSHARIDAAEGPSDIPD 156

RESULT 2  
 CDNS\_MOUSE STANDARD; PRT; 130 AA.

DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DE 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE CYCLIN-DEPENDENT KINASE 4 INHIBITOR B (P14-INK4B) (P15-INK4B).  
 GN CDKN2B.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95380169; PubMed=7651726;  
 RA Quelle D.E., Ashmun R.A., Hannon G.J., Rehberger P.A., Trono D.,  
 RA Richter K.H., Walker C., Beach D., Sherr C.J., Serrano M.;  
 RT "Cloning and characterization of murine p16INK4a and p15INK4b genes.";  
 RL Oncogene 11:635-645(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J X DBA;  
 RX MEDLINE=973222242; PubMed=9178896;  
 RA Malumbres M., de Castro I., Santos J., Melendez B., Manges R.,  
 RA Serrano M., Pellicer A., Fernandez-Piqueras J.;  
 RT "Inactivation of the cyclin-dependent kinase inhibitor p15INK4b by  
 RT deletion and de novo methylation with independence of p16INK4a  
 RT alterations in murine primary T-cell lymphomas.";  
 RP Oncogene 14:1361-1370(1997).  
 CC -!- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHIBITOR.  
 CC POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL CYCLE ARREST (BY  
 CC SIMILARITY).  
 CC -!- SUBUNIT: HETERODIMER OF P14 WITH CDK4 (BY SIMILARITY).  
 CC -!- TISSUE SPECIFICITY: EXPRESSED UBIQUITOUSLY.  
 CC -!- INDUCTION: BY TGF-BETA.  
 CC -!- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE  
 CC INHIBITORS.  
 CC -!- SIMILARITY: CONTAINS 4 ANK REPEATS.

-----  
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 CC -----  
 DR EMBL; U66085; AAB39833.1; -  
 DR EMBL; U66084; AAB39833.1; JOINED.  
 DR MGD; MGI:104737; Cdkn2b.  
 DR InterPro; IPR002110; -  
 DR Pfam; PF00203; ank; 3.  
 DR PROSITE; PS50088; ANK\_REPEAT; 1.  
 DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.

Cell cycle; Anti-oncogene; Repeat; ANK repeat.  
 FT REPEAT 5 34 ANK 1.  
 FT REPEAT 38 66 ANK 2.  
 FT REPEAT 71 100 ANK 3.  
 FT REPEAT 104 130 ANK 4.  
 SQ SEQUENCE 130 AA; 13788 MW; 7AAD60FF552BCFF9 CRC64;

Query Match 66.1%; Score 529; DB 1; Length 130;  
 Best Local Similarity 88.3%; Pred. No. 2.8e-42;  
 Matches 106; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 16 LATAAARGVVEEVRALLLEAVLNPAPNSYGRRPITQVMMGSAVAELLLHGAEPNCADP 75  
 Db 10 LATAAARGQVETVRLLEAGADNALNRFRPITQVMMGSAQVAELLLHGAEPNCADP 69

QY 76 ATLTPRVHDAAREGFLDTLVVLRHAGARLDVDRWAGRLPVDIAEEGLHGRDVARVYLRRAAG 135  
 Db 70 ATLTPRVHDAAREGFLDTLVVLRHAGARLDVCDWAGRLPVDIAEEQGRDIARYLHAAYG 129

RESULT 3  
 CDNS\_HUMAN STANDARD; PRT; 138 AA.

DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DE 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE CYCLIN-DEPENDENT KINASE 4 INHIBITOR B (P14-INK4B) (P15-INK4B)  
 DE (MULTIPLE TUMOR SUPPRESSOR 2) (MTS2).  
 GN CDKN2B OR MTS2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95095079; PubMed=8001816;  
 RA Guan K.-L., Jenkins C.W., Li Y., Nichols M.A., Wu X., O'Keefe C.L.,  
 RA Matera G.A., Xiong Y.;  
 RT "Growth suppression by p18, a p16INK4/MTS1- and p14INK4B/MTS2-related  
 RT CDK6 inhibitor, correlates with wild-type pRb function.";  
 RL Genes Dev. 8:2939-2952(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94359613; PubMed=8078588;  
 RA Hannon G.J., Beach D.;  
 RT "p15INK4B is a potential effector of TGF-beta-induced cell cycle  
 RT arrest.";  
 RL Nature 371:257-261(1994).  
 RN [3]  
 RP SEQUENCE OF 53-138 FROM N.A.  
 RX MEDLINE=94204645; PubMed=8153634;  
 RA Kamb A., Gruis N.A., Weaver-Feldhaus J., Liu Q., Harshman K.,  
 RA Tavtigian S.V., Stockert E., Day R.S. III, Johnson B.E.,  
 RA Skolnick M.H.;  
 RT "A cell cycle regulator potentially involved in genesis of many tumor  
 RT types.";  
 RL Science 264:436-440(1994).  
 RN [4]  
 RP VARIANTS LUNG ADENOCARCINOMA GLU-47 AND VAL-50.  
 RX MEDLINE=95188190; PubMed=782351;  
 RA Okamoto A., Hussain S.P., Hagiwara K., Spillare E.A., Rusin M.R.,  
 RA Demetrick D.J., Serrano M., Hannon G.J., Shiseki M., Zariwala M.,  
 RA Xiong Y., Beach D.H., Yokota J., Harris C.C.;  
 RT "Mutations in the p16INK4/MTS1/CDKN2, p15INK4B/MTS2, and p18 genes in  
 RT primary and metastatic lung cancer.";  
 RL Cancer Res. 55:1448-1451(1995).  
 CC -!- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHIBITOR.  
 CC POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL CYCLE ARREST.  
 CC -!- SUBUNIT: HETERODIMER OF P14 WITH CDK4.  
 CC -!- DISEASE: CDKN2B MUTATIONS ARE INVOLVED IN TUMOR FORMATION.  
 CC -!- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE

Cancer Res. 55:1607-1612(1995).

-!- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHIBITOR.  
POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL CYCLE ARREST (BY  
SIMILARITY).  
-!- SUBUNIT: HETERODIMER OF p14 WITH CDK4.  
-!- ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY ALTERNATIVE  
INITIATION CODONS IN THE SAME READING FRAME.  
-!- TISSUE SPECIFICITY: EXPRESSION ABUNDANT IN LUNG, LESS ABUNDANT IN  
TESTIS, BARELY DETECTABLE IN LIVER, AND NOT DETECTABLE IN NEONATAL  
KIDNEY, ADULT KIDNEY, BRAIN, HEART, OR SPLEEN.  
-!- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE  
INHIBITORS.  
-!- SIMILARITY: CONTAINS 4 ANK REPEATS.

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EMBL; S79760; AAB35360.1; -.  
DR EMBL; S77734; -. NOT\_ANNOTATED\_CDS.  
DR InterPro; IPR002110; -.  
DR Pfam; PF00023; ank; 3.  
DR PROSITE; PS50088; ANK\_REPEAT; 1.  
DR PROSITE; PS50297; ANK\_REP\_REGION; 1.  
KW Cell cycle; Anti-oncogene; Repeat; ANK repeat; Alternative initiation.  
FT CHAIN 1 130 CYCLIN-DEPENDENT KINASE 4 INHIBITOR B,  
FT LONG ISOFORM.  
FT CHAIN 46 130 CYCLIN-DEPENDENT KINASE 4 INHIBITOR B,  
FT SHORT ISOFORM.  
FT INIT MET 46 46 FOR SHORT ISOFORM.  
FT REPEAT 5 34 ANK 1.  
FT REPEAT 38 66 ANK 2.  
FT REPEAT 71 100 ANK 3.  
FT REPEAT 104 130 ANK 4.  
FT SEQUENCE 130 AA; 13748 MW; AC45B21FA69FAD92 CRC64;

Query Match 65.5%; Score 524; DB 1; Length 130;  
Best Local Similarity 86.7%; Pred. No. 8e-42;  
Matches 104; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 16 LATAAARGRVEVRALLAEVALPNAPNSYGRRPQIVMMGMSARVAEELLHLGAEPNCADP 75  
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Db 10 LATAAARGQVETRVQLLEGADPNNAVRFGRPPQIVMMGMSAQVAEELLHLGAEPNCADP 69  
  
QY 76 ATLTPRVHDAAEGFDLTVLVLRAGARGLDVRDAWGRLPVDLAEEGLGHDRVARYLRAAAG 135  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:  
Db 70 ATLTPRVHDAAEGFDLTMLVLRAGARGLDCDANGRLPVDLAEEGGHRDIARYLHAATG 129

RESULT 5  
CDN2\_MOUSE  
ID CDN2\_MOUSE STANDARD; PRT; 167 AA.  
AC F51480;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I) (P16-INK4) (P16-INK4A).  
GN CDKN2A OR P16INK4A.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
CB NCBI\_Taxid=10090;  
RN [1]  
RS SEQUENCE FROM N.A.  
RX MEDLINE=95380169; PubMed=7651726;  
RA Quelle D.E., Ashmun R.A., Hannon G.J., Rehberger P.A., Trono D.,  
RA Richter K.H., Walker C., Beach D., Sherr C.J., Serrano M.:  
NT "Cloning and characterization of murine p16INK4a and p15INK4b genes.";

CC		INHIBITORS.
CCC	-I-	SIMILARITY: CONTAINS 2 ANK REPEATS.
CC		-----
CCC		This SWISS-PROT entry is copyright. It is produced through a collaboration
CC		between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CCC		or send an email to licenseseis@sib-sib.ch).
CC		-----
DNR	EMBL;	U17075; RAC50075.1; --
CC	EMBL;	L36844; ARA50282.1; --
CC	EMBL;	S69805; RAD14049.1; --
DNR	MIM;	G00431; --
DNR	PROSITE;	PS0297; ANK_REP_REGION; 1.
KW	Cell cycle;	Anti-oncogene; Repeat; ANK repeat; Disease mutation.
DDR	REPEAT	13 39 ANK 1 (INCOMPLETE).
FT	REPEAT	13 103 ANK 2.
FT	VARIANT	47 47 G>>E (IN LUNG ADENOCARCINOMA).
		/FTID=VAR_001488.
	VARIANT	50 50 A->V (IN LUNG ADENOCARCINOMA).
		/FTID=VAR_001489.
FT	CONFLICT	20 21 SA->TP (IN REF. 2).
FT	CONFLICT	23 23 MISSING (IN REF. 2).
FT	CONFLICT	32 34 QLL->HSW (IN REF. 2).
SQ	SEQUENCE	138 AA; 14722 MW; OD6FFBFA6FEAD21 CRC64;
	Query Match	65.8%; Score 526; DB 1; Length 138;
	Best Local Similarity	82.0%; Pred. No. 5.6e-42;
	Matches 109; Conservative	4; Mismatches 16; Indels 4; Gaps 1;
QY	3	PAAGSMPEPSDWLTAAARGVEEVRLLEAVLPNAPNSVGRRPIQVMNGSARVAEL 62
	I:-	
Db	9	PSGGSDSE----GLASAAAGLVKEVKQLLEGADGNGVRFGRRAIQVMNGSARVAEL 64
	I:	
QY	63	LLLHGAEPNCADPATLPFPHVDAAAREGFDTLVVLHRAGARLDVRDANGRLPVDLAEBLG 122
	I:	
Db	65	LLLHGAEPNCADPATLPFPHVDAAAREGFDTLVVLHRAGARLDVRDANGRLPVDLAEBRG 124
	I:	
QY	123	HRDVARYLRAAAG 135
	I:	I
Db	125	HRDVAGYLRTATG 137
	I:	I
	RESULT 4	
	CDS_RAT	STANDARD; PRT; 130 AA.
	CDNS_RAT	P55272;
	DT	01-OCT-1996 (Rel. 34, Created)
DT	DT	01-OCT-1996 (Rel. 34, Last sequence update)
DT	DT	01-OCT-2000 (Rel. 40, Last annotation update)
DE	DE	CYCLIN-DEPENDENT KINASE 4 INHIBITOR B (P14-INK4B) (P15-INK4B).
GN	GN	CDKN2B OR INK4.
OS	OS	Rattus norvegicus (Rat).
OC	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX	OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxId	NCBI_TaxId	=10116;
[1]	[1]	SEQUENCE FROM N.A.
RP	RP	MEDLINE=96001392; PubMed=7546221;
RX	RX	Hino O., Kobayashi E., Hirayama Y., Kobayashi T., Kubo Y.,
RA	RA	Tsuchiya H., Kikuchi Y., Mitani H.;
RT	RT	"Molecular genetic basis of renal carcinogenesis in the Eker rat
RT	RT	model of tuberosc sclerosis (Tsc2).";
RL	RL	Mol. Carcinog. 14:23-27(1995).
RN	RN	[2]
RP	RP	SEQUENCE OF 46-86 FROM N.A.
RX	RX	MEDLINE=95228036; PubMed=7712460;
RA	RA	Knapek D.F., Serrano M., Beach D., Trono D., Walker C.L.;
RT	RT	"Association of rat p15INK4B/p16INK4 deletions with monosomy 5 in
RT	RT	kidney epithelial cell lines but not primary renal tumors.";

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CC ABILITY TO INTERACT WITH CYCLINS D. COULD ACT AS A NEGATIVE
CC REGULATOR OF THE PROLIFERATION OF NORMAL CELLS (BY SIMILARITY).
CC -!- SUBUNIT: HETERODIMER WITH CDK4 OR CDK6 (BY SIMILARITY).
CC -!- ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY ALTERNATIVE
CC INITIATION CODONS IN THE SAME READING FRAME.
CC -!- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
CC INHIBITORS.
CC -!- SIMILARITY: CONTAINS 3 ANK REPEATS.
CC -----
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CC -----
CC EMBL; AF064808; AAC23669.1; -.
CC EMBL; AF064808; AAC23670.1; -.
CC InterPro: IPR002110; -.
CC Pfam: PF00023; ank, 3.
CC PROSITE; PS00088; ANK_REPEAT; 1.
CC PROSITE; PS0297; ANK_REPEAT_REGION; 1.
CC KW Cell cycle; Anti-oncogene; Repeat; ANK repeat; Alternative initiation.
CC FT CHAIN 1 171 CYCLIN-DEPENDENT KINASE 4 INHIBITOR A,
CC FT FT LONG ISOFORM.
CC FT CHAIN 35 171 CYCLIN-DEPENDENT KINASE 4 INHIBITOR A,
CC FT FT SHORT ISOFORM.
CC FT INIT_MET 35 35 FOR SHORT ISOFORM.
CC FT REPEAT 45 74 ANK 1.
CC FT REPEAT 78 106 ANK 2.
CC FT REPEAT 111 140 ANK 3.
CC SEQUENCE 171 AA; 18707 MW; 694264F5D0F4F6CC CRC64;
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Query Match 51.0%; Score 408; DB 1; Length 171;
Best Local Similarity 69.2%; Pred. No. 5.5e-31;
Matches 83; Conservative 9; Mismatches 28; Indels 0; Gaps 0;
QY 12 SADWLATAAARGVEEYRALLEAVALEPNAPNSYGRPRPIQVMMGSAFVAEILLHLGAEPN 71
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
46 SGEKLTEAARGTEVTELELGTNPNVNRGSAIQVMMGNVRLAAIILQYGAEPN 105
QY 72 CADPATLTREPVHDAAREGFDTLVLHHRAGARLDVRDAGWGLPVDLAEELGHRDVARYL 131
Db || || || || || || || || || || || || || || || || || || || || ||
106 TPDPDTLTLPVHDAAREGFDTLMLLHRAGARLDVRDWSGRLPVDLAEEOGHHLVVAYLR 165
RESULT 7
CDN7_HUMAN STANDARD; PRT; 166 AA.
AC P55273; Q13102;
AD 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 01-OCT-2000 (Rel. 40, Last annotation update)
DE CYCLIN-DEPENDENT KINASE 4 INHIBITOR D (P19-INK4D).
GN CDKN2D.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=96121373; PubMed=8575754;
RA Okuda T., Hirai H., Valentine V.A., Shurtleff S.A., Kidd V.J.,
RA Lahti J.M., Sherr C.J., Downing J.R.;
RT "Molecular cloning, expression pattern, and chromosomal localization
RT of human CDKN2D/INK4d, an inhibitor of cyclin D-dependent kinases.";
RL Genomics 29:633-630(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96362662; PubMed=8741839;

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FT REPEAT 138 166 ANK 3.
FT CONFLICT 17 A -> P (IN REF. 2).
SQ SEQUENCE 166 AA: 17894 MW: 9E74F5C23B7EBCB2 CRC64;

Query Match 31.1%; Score 249; DB 1; Length 166;
Best Local Similarity 44.3%; Pred. No. 2.5e-16;
Matches 70; Conservative 18; Mismatches 52; Indels 18; Gaps 5;

QY 14 DWLATAAAGRVEEVRALL-TAVALPNAPNSYGRRPQVMMGMSARVAEILLHLHGAEPNC 72
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Db 10 DRUSGARAGDQVQVRRLLHRELVHPDNLNFGKTAQVMFGSPAVALLELLKQGASPMV 69
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QY 73 ADPATLTRPVHDAAREGFELTLVLHRAGARLDVYRDAGRLPVDLAEELCHRDVARYL-- 130
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Db 70 QD-ASCTSPVHDAARTGLDTLKLVLVEHGDVYDNLDTGSLPLTHLAIREGHSSVVSFLAP 128
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QY 131 -----RAAGGT-----RCSNHKARIDAAEGPSDIP 155
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Db 129 ESDLHRDASGLTLELARQGAQNL-MDILQGHMWP 165
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RESULT 9
CDN6_MOUSE
ID CDN6_MOUSE STANDARD; PRT; 168 AA.
AC O60772:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) (CYCLIN-DEPENDENT
DE KINASE 4 INHIBITOR C) (P18-INK4C).
DE CDKN2C.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_Taxid=10090;
RN [1]
RS SEQUENCE FROM N.A.
RC STRAIN=C57BL KAPLAN;
RX MEDLINE=95257948; PubMed=7739547;
RA Hirai H., Rousset M.P., Kato J.-Y., Ashmun R.A., Sherr C.J.;
RT "Novel INK4 proteins, p19 and p18, are specific inhibitors of the
RT cyclin D-dependent kinases CDK4 and CDK6.";
RL Mol. Cell. Biol. 15:2672-2681(1995).
CC -1- FUNCTION: INTERACTS STRONGLY WITH CDK6, WEAKLY WITH CDK4. INHIBITS
CC CELL GROWTH AND PROLIFERATION WITH A CORRELATED DEPENDENCE ON
CC ENDOGENOUS RETINOBLASTOMA PROTEIN RB.
CC -1- SUBUNIT: HETERODIMER OF P18 WITH CDK6 (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
CC INHIBITORS.
CC -1- SIMILARITY: CONTAINS 5 ANK REPEATS.
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CC EMBL; U19596; AAC52193.1; --
CC MGD; MGI:105388; Cdkn2c.
CC InterPro; IPR002110; --
CC Pfam; PF00023; ank; 3.
CC PROSITE; PS5088; ANK_REPEAT; 2.
CC PROSITE; PS50297; ANK_REPEAT_REGION; 1.
CC Cell cycle; Repeat; ANK repeat.
CC REPEAT 4 33 ANK 1.
CC REPEAT 37 65 ANK 2.
CC REPEAT 69 98 ANK 3.
CC REPEAT 102 132 ANK 4.
CC REPEAT 136 165 ANK 5.
CC SEQUENCE 168 AA; 18066 MW; BC88B5489307E128 CRC64;

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FT REPEAT 129 158 ANK 3.
FT REPEAT 162 191 ANK 4.
FT REPEAT 193 220 ANK 5.
FT REPEAT 232 261 ANK 6.
FT REPEAT 265 294 ANK 7.
FT REPEAT 298 327 ANK 8.
FT REPEAT 331 360 ANK 9.
FT REPEAT 364 393 ANK 10.
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FT REPEAT 430 459 ANK 12.
FT REPEAT 463 492 ANK 13.
FT REPEAT 496 525 ANK 14.
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FT REPEAT 4753 4785 ANK 137.
FT REPEAT 4788 4820 ANK 138.
FT REPEAT 4823 4855 ANK 139.
FT REPEAT 4858 4890 ANK 140.
FT REPEAT 4893 4925 ANK 141.
FT REPEAT 4928 4960 ANK 142.
FT REPEAT 4963 4995 ANK 143.
FT REPEAT 4998 5030 ANK 144.
FT REPEAT 5033 5065 ANK 145.
FT REPEAT 5068 5100 ANK 146.
FT REPEAT 5103 5135 ANK 147.
FT REPEAT 5138 5170 ANK 148.
FT REPEAT 5173 5205 ANK 149.
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FT REPEAT 16283 16315 ANK 466.
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FT REPEAT 17228 17260 ANK 493.
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FT REPEAT 17438 17470 ANK 499.
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FT REPEAT 18073 18105 ANK 517.
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FT REPEAT 18738 18770 ANK 536.
FT REPEAT 18773 18805 ANK 537.
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FT REPEAT 18843 18875 ANK 539.
FT REPEAT 18878 18910 ANK 540.
FT REPEAT 18913 18945 ANK 541.
FT REPEAT 18948 18980 ANK 542.
FT REPEAT 18983 19015 ANK 543.
FT REPEAT 19018 19050 ANK 544.
FT REPEAT 19053 19085 ANK 545.
FT REPEAT 19088 19120 ANK 546.
FT REPEAT 19123 19155 ANK 547.
FT REPEAT 19158 19190 ANK 548.
FT REPEAT 19193 19225 ANK 549.
FT REPEAT 19228 19260 ANK 550.
FT REPEAT 19263 19295 ANK 551.
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FT REPEAT 19683 19715 ANK 563.
FT REPEAT 19718 19750 ANK 564.
FT RE
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FT VARIANT 462 462 /FTid-VAR_000595.
FT V -> I (IN HS).
FT /FTid-VAR_000596.
FT R -> H (IN BRUEGGEN).
FT /FTid-VAR_000597.
FT V -> A.
FT /FTid-VAR_000598.
FT D -> E.
FT /FTid-VAR_000599.
FT S -> T.
FT /FTid-VAR_000600.
FT E -> D.
FT /FTid-VAR_000601.
FT D -> N (IN DUESSELDORF).
FT /FTid-VAR_000602.
FT R -> D.
FT /FTid-VAR_000603.
FT CONFLICT 229 229 A -> S (IN REF. 2).
FT CONFLICT 1545 1545 V -> I (IN REF. 2).
FT SEQUENCE 1880 AA; 206145 MW; 1C5F5E7EFDICD428 CRC64;

Query Match 16.7%; Score 133.5; DB 1; Length 1880;
Best Local Similarity 35.4%; Pred. No. 0.00017;
Matches 52; Conservative 15; Mismatches 69; Indels 11; Gaps 6;

QY 16 LATAAARGVEEVRALLAEVALPNAPNSYGRRPQV-MMGSGARVAELLLHGAEPNCAD 74
DB 506 LHIAAREGHVETLALLEKEASQACMTKGTPLHVAAYKGVKVAELLLERDAHPNAAG 565

QY 75 PATITREPVHDAAREGFDLT-L-VVLHAGARLDVRDAW-GELPVDLAEELGHRDVARYL-- 130
DB 566 KNGLT-PLHVAVHNNLDIVKLLPRGGS--PHSPAWNGYTPHIAAKQNOVEVARSLQ 622

QY 131 ---RAAAGTGRGNHARIDAAEGPSDI 154
DB 623 YGGSANAEVQGVTPHLHAAQEGHAEM 649

RESULT 14
DAPK_HUMAN STANDARD; PRT; 1431 AA.
AC P53355;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE DPATH-ASSOCIATED PROTEIN KINASE 1 (EC 2.7.1.-) (DAP KINASE 1).
GN DAPK1 OR DAPK.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95129831; PubMed=7828849;
RA Deiss L.P., Feinstein E., Berissi H., Cohen O., Kimchi A.;
RT "Identification of a novel serine/threonine kinase and a novel 15-kD
RT protein as potential mediators of the gamma interferon-induced cell
RT death.";
RL Genes Dev. 9:15-30(1995).
RN [2]
RP REVISIONS TO 164-171.
RA Feinstein E.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INVOLVED IN MEDIATING INTERFERON-GAMMA-INDUCED CELL
CC DEATH.
CC -!- PTM: AUTOPHOSPHORYLATED.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -!- SIMILARITY: CONTAINS 10 ANK REPEATS.
CC -!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X76104; CAA53712.1; -.
DR HSP; Q63450; IA06.
DR MIM; 600831; -.
DR InterPro; IPR000488; -.
DR InterPro; IPR000719; -.
DR InterPro; IPR002110; -.
DR InterPro; IPR002290; -.
DR Pfam; PF00023; ank; 8.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00069; pkinase; 1.
DR PROSITE; PS50088; ANK_REPEAT; 6.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS50107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS50108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
KW Phosphorylation; ATP-binding; Repeat; ANK repeat; Apoptosis.
FT DOMAIN 13 266 PROTEIN KINASE.
FT DOMAIN 267 334 CALMODULIN-BINDING.
FT REPEAT 378 407 ANK 1.
FT REPEAT 411 440 ANK 2.
FT REPEAT 444 473 ANK 3.
FT REPEAT 478 507 ANK 4.
FT REPEAT 511 540 ANK 5.
FT REPEAT 544 573 ANK 6.
FT REPEAT 577 606 ANK 7.
FT REPEAT 610 639 ANK 8.
FT REPEAT 676 705 ANK 9.
FT REPEAT 1163 1197 ANK 10.
FT DOMAIN 1313 1397 DEATH.
FT NP_BIND 19 27 ATP (BY SIMILARITY).
FT BINDING 42 42 ATP (BY SIMILARITY).
FT ACT_SITE 139 139 BY SIMILARITY.
FT MUTAGEN 42 42 K->A: LOSS OF ACTIVITY.
SQ SEQUENCE 1431 AA; 160017 MW; 9E84811004A155B CRC64;

Query Match 16.3%; Score 130.5; DB 1; Length 1431;
Best Local Similarity 29.1%; Pred. No. 0.00024;
Matches 44; Conservative 14; Mismatches 54; Indels 39; Gaps 4;

QY 16 LATAAARGVEEVRALLAEVALPNAPNSYGRRPQVMMGSGAR----VAEILLHGAEPN 71
DB 483 LHCAAWHGYSYVAKALCEAGCNVNIKNEGETP---LLTASARGYHDIVECLAERGADLN 539

QY 72 CADP-----ATL-----TRPVHDAAREGFDLT-LVVLHR 99
DB 540 ACDKDGHTALHLAVRRCOMEVIKTLSSQCFVDYQDRHGNTPLHVACKDGNMPTVALCE 599

QY 100 AGARLDVRDAMGRPLPVDLAEELGHRDVARYL 130
DB 600 ANCNLDISNKKYGRTPHLHAAANNGLDVVRYL 630

RESULT 15
NTC4_MOUSE
ID NTC4_MOUSE STANDARD; PRT; 1964 AA.
AC P31695; Q62389;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING
DE PROTEIN INT-3).
GN NOTCH4 OR INT3 OR INT-3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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FT	DISULFID	595	610	BY SIMILARITY.
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FT	DISULFID	676	685	BY SIMILARITY.
FT	DISULFID	692	703	BY SIMILARITY.
FT	DISULFID	697	712	BY SIMILARITY.
FT	DISULFID	714	723	BY SIMILARITY.
FT	DISULFID	730	741	BY SIMILARITY.
FT	DISULFID	735	750	BY SIMILARITY.
FT	DISULFID	752	761	BY SIMILARITY.
FT	DISULFID	768	779	BY SIMILARITY.
FT	DISULFID	773	788	BY SIMILARITY.
FT	DISULFID	790	799	BY SIMILARITY.
FT	DISULFID	807	818	BY SIMILARITY.
FT	DISULFID	812	827	BY SIMILARITY.
FT	DISULFID	829	838	BY SIMILARITY.
FT	DISULFID	845	856	BY SIMILARITY.
FT	DISULFID	850	865	BY SIMILARITY.
FT	DISULFID	867	876	BY SIMILARITY.
FT	DISULFID	882	903	BY SIMILARITY.
FT	DISULFID	897	912	BY SIMILARITY.
FT	DISULFID	914	923	BY SIMILARITY.
FT	DISULFID	930	941	BY SIMILARITY.
FT	DISULFID	935	950	BY SIMILARITY.
FT	DISULFID	952	961	BY SIMILARITY.
FT	DISULFID	968	979	BY SIMILARITY.
FT	DISULFID	973	988	BY SIMILARITY.
FT	DISULFID	990	999	BY SIMILARITY.
FT	DISULFID	1006	1019	BY SIMILARITY.
FT	DISULFID	1011	1028	BY SIMILARITY.
FT	DISULFID	1030	1039	BY SIMILARITY.
FT	DISULFID	1046	1057	BY SIMILARITY.
FT	DISULFID	1051	1069	BY SIMILARITY.
FT	DISULFID	1071	1080	BY SIMILARITY.
FT	DISULFID	1087	1098	BY SIMILARITY.
FT	DISULFID	1092	1110	BY SIMILARITY.
FT	DISULFID	1112	1121	BY SIMILARITY.
FT	DISULFID	1130	1142	BY SIMILARITY.
FT	DISULFID	1136	1155	BY SIMILARITY.
FT	DISULFID	1157	1166	BY SIMILARITY.
Query Match 15.6%; Score 125; DB 1; Length 1964;				
Best Local Similarity 25.5%; Pred. No. 0.0011;				
Matches 52; Conservative 16; Mismatches 66; Indels 70; Gaps 5;				
16 LATAAARGVEEVALLLEAVALPNAPNSYGRFPQVMMGSAR-VAEELL----- 64				
1633 LHAAARFSRPTAARRLLEAGANPNQPDAGRTPLHTAADAAREVCQLLLASRQTSVDAR 1692				
Db	1633	LHAAARFSRPTAARRLLEAGANPNQPDAGRTPLHTAADAAREVCQLLLASRQTSVDAR 1692		
Qy	65	-----LH-----G 67		
Db	1693	TEDGTTPLMLAARLAVEDLVEELIAARADYGARDKRGKGTALHMAAAVNNARAARSLQAG 1752		
Qy	68	AEPNCADPATLTPRVHDAAREGFLDTLVLRHAGARLDVRDAGRLPVDLAEELGHRDVA 127		
Db	1753	ADKDAQSREGT-PLFLAAREGAVEVAQLLELGAARGLRDQAGLAPGCVARORSHWDL 1811		
Qy	128	RYLRAAAGGTRGSN-HARIDAAEG 150		
Db	1812	TLLEGAGTTQEARAHARTTPGGG 1835		



Result No.	Query Match	Score	Query			ID	Description
			Match	Length	DB		
1	68.5	548	106	4	Q9NP05	Q9np05 homo sapien	
2	63.8	510	157	11	Q9EQ33	Q9eq33 mesocricetū	
3	59.6	476.5	159	11	Q9R0Z3	Q9r0z3 rattus norv	
4	476	395.5	168	11	P97510	P97510 mus musculu	
5	474	392.1	168	11	O89088	O89088 mus musculu	
6	449	361.1	102	6	Q9XS11	Q9xs11 felis silve	
7	444	355.5	103	6	Q9TSY1	Q9tsy1 sus scrofa	
8	427	343	86	6	Q9XS52	Q9xs52 felis silve	
9	409	311	81	6	Q9GMR2	Q9gm2 canis famil	
10	408	310	86	11	Q9Z1C1	Q9z1c1 mus spretus	
11	408	310	86	11	Q9QUP0	Q9qup0 mus musculu	
12	407	309	86	6	Q9TSY0	Q9tsy0 sus scrofa	
13	405	306	86	11	O54846	O54846 mus musculu	
14	334	314.8	113	11	Q9Z1C2	Q9z1c2 mus musculu	
15	331	314	113	11	Q9QWH5	Q9qwh5 mus musculu	
16	327	309	113	11	Q9QWH8	Q9qwh8 mus musculu	
17	326	308	113	11	Q9QWH7	Q9qwh7 mus musculu	
18	326	308	113	11	Q9QWH6	Q9qwh6 mus musculu	
19	314.5	39.3	112	11	Q9QWH4	Q9qwh4 mus musculu	

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RESULT 2
Q9EQ33 ID Q9EQ33 PRELIMINARY; PRT; 157 AA.
AC Q9EQ33;
DT 01-MAY-2000 (TREMBLrel. 16, Created)
DT 01-MAY-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE CYCLIN DEPENDENT KINASE INHIBITOR 2.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
SEQUENCE FROM N.A.
RA Muscarella P., Knobloch T.J., Weghorst C.M.;
RA "Sequencing of the Syrian Golden Hamster CDKN2/MTS1 Gene and
RT Identification of Inactivating Alterations in Hamster Tumor Cell
RT Lines."
RT Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
SQ EMBL; AF292567; AAG4950.1; -.
SQ SEQUENCE 157 AA; 16635 MW; 06FD66AE6B30DCF8 CRC64;

Query Match 63.8%; Score 510; DB 11; Length 157;
Best Local Similarity 68.9%; Pred. No. 8.9e-37;
Matches 102; Conservative 17; Mismatches 29; Indels 0; Gaps 0;

QY 9 MEPSADWLATAAARGRVEEVRALLEVALPNAPNSYGRRPQVMMGMSARVAELLHLHGA 68
DB 1 MEPSADGLARAAGRGREHVRALLEAGASNPNTFTPIQVMMGNVVAALLLSYGA 60

QY 69 EPNCADPATLTRPVHDAAREGFDTLVHLRAGARLDVDRDAGRLPVDLAEEELGHRDVAR 128
DB 61 EPNCEDPATLSRPVHDAAREGFDTLVHLRAGARLDVDRDAGRLPVDLALERGHHDVVR 120

QY 129 YLRAAGGTGRGSHARIDAAEGSPDIP 156
DB 121 YLRAAGNTPOGSEPGAGVTSQAQTPPEVSD 148

RESULT 3
Q9R023 ID Q9R023 PRELIMINARY; PRT; 159 AA.
AC Q9R023;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE P16 PROTEIN P16INK4A.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RA STRAIN=F344/N; TISSUE=LUNG;
RA MEDLINE=97184461; PubMed=9032263;
RA Swafford D.S., Middleton S.K., Palmisano W.A., Nikula K.J.,
RA Tesfalgzi J., Baylin S.B., Herman J.G., Belinsky S.A.;
RA "Frequent aberrant methylation of p16INK4a in primary rat lung
RT tumors."
RL Mol. Cell. Biol. 17:1366-1374(1997).
DR EMBL; L81167; AAD48924.1; -.
DR HSPF; Q60773; IAP7.
DR InterPro; IPR002110; -.
DR Pfam; PF00023; ank; 4.
DR PROSITE; PS0297; ANK_REP_REGION; 1.
DR SMART; SM00248; ANK; 1.
SQ SEQUENCE 159 AA; 17366 MW; 3C4CA920A1FEAE6B CRC64;

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Query Match 59.6%; Score 476.5; DB 11; Length 159;

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Best Local Similarity 74.6%; Pred. No. 7e-34;
Matches 97; Conservative 11; Mismatches 19; Indels 3; Gaps 1;

QY 9 MEPSADWLATAAARGRVEEVRALLEVALPNAPNSYGRRPQVMMGMSARVAELLHLHGA 68
DB 1 MEPSADGLARAAGRGREHVRALLEAGASNPNTFTPIQVMMGNVVAALLLSYGA 60

QY 69 EPNCADPATLTRPVHDAAREGFDTLVHLRAGARLDVDRDAGRLPVDLAEEELGHRDVAR 128
DB 61 EPNCEDPATLSRPVHDAAREGFDTLVHLRAGARLDVDRDAGRLPVDLALERGHHDVVR 120

QY 129 YLRAAGGTGRGSHARIDAAEGSPDIP 135
DB 121 YLRYLLSSAG 130

RESULT 4
P97510 ID P97510 PRELIMINARY; PRT; 168 AA.
AC P97510; p97937;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE CYCLIN DEPENDENT KINASE INHIBITOR P16INK4A (P16INK4A TUMOR SUPPRESSOR
DE PROTEIN) (CYCLIN DEPENDENT KINASE INHIBITOR 2A) (P16INK4A) (CYCLIN-
DE DEPENDENT KINASE INHIBITOR PROTEIN).
GN CDKN2A OR E1ALPHA OR P16INK4A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RA STRAIN=DBA/2N; TISSUE=SPLEEN;
RA MEDLINE=98151529; PubMed=9482902;
RA Zhang S., Ramsay E.S., Mock B.A.;
RA "CDKN2a, the cyclin-dependent kinase inhibitor encoding p16INK4a and
RT p19ARF, is a candidate for the plasmacytoma susceptibility locus,
RT Pctrl."
RL Proc. Natl. Acad. Sci. U.S.A. 95:2429-2434(1998).
RN [2]
SEQUENCE OF 1-42 FROM N.A.
RP STRAIN=VARIOUS STRAINS;
RC MEDLINE=97179476; PubMed=9021155;
RA Herzog C.R., You M.;
RT "Sequence variation and chromosomal mapping of the murine Cdkn2a tumor
RL suppressor gene."
RL Mamm. Genome 8:65-66(1997).
RN [3]
SEQUENCE OF 1-155 FROM N.A.
RC STRAIN=C57BL/6J X DBA;
RA Malumbres M., de Castro I., Santos J., Melendez B., Mangueres R.,
RA Serrano M., Pellicer A., Fernandez-Piqueras J.;
RA Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
SEQUENCE OF 1-42 FROM N.A.
RP STRAIN=DBA/2, AND C57BL/6;
RC MEDLINE=95380169; PubMed=7651726;
RA Queller D.E., Ashmun R.A., Hannon G.J., Rehberger P.A., Trono D.,
RA Richter K.H., Walker C., Beach D., Sherr C.J., Serrano M.;
RA "Cloning and characterization of murine p16INK4a and p15INK4b genes."
RL Oncogene 11:635-645(1995).
RN [5]
SEQUENCE OF 1-42 FROM N.A.
RP STRAIN=DBA/2, AND C57BL/6;
RC Gressani K.M., Rollins L.A., Miller M.S.;
RA Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [6]
SEQUENCE OF 1-11 FROM N.A.
RP STRAIN=ICR SWISS;
RC MEDLINE=97128829; PubMed=8973369;
RA Soloff E.V., Herzog C.R., You M.;
RT "The 5'-flanking region of the E1 alpha form of the murine p16INK4a

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RT (MTS1) gene.";  
RL Gene 180:213-215(1996).  
RN [7]  
RP SEQUENCE OF 1-42 FROM N.A.  
RC STRAIN=CAST/EI, C57BL/6J, ARF/J, AND MOLF/EI;  
RA Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M.,  
RA Pellicer A., Fernandez-Piqueras J.;  
RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences  
in mouse inbred strains";  
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF044336; AAC08963.1; -  
DR EMBL; U49280; AAC00052.1; -  
DR EMBL; U66087; AAB39600.1; -  
DR EMBL; U66086; AAB39600.1; JOINED.  
DR EMBL; AF004588; AAB61416.1; -  
DR EMBL; U47018; AAC52987.1; -  
DR EMBL; U79628; AAD00226.1; -  
DR EMBL; U79625; AAD00223.1; -  
DR EMBL; U79627; AAD00225.1; -  
DR HSSP; P42771; 1BI7.  
MGD; MGI:104738; Cdkn2a.  
InterPro: IPR002110; -  
DR Pfam; PF00023; ank; 4.  
DR PROSITE; PS50297; ANK_REP_REGION; 1.  
DR SMART; SM00248; ANK; 1.  
KW Kinase; Cyclin.  
SQ SEQUENCE 168 AA; 17941 MW; 9A6B0F24F34D5FEC CRC64;  
  
Query Match 59.5%; Score 476; DB 11; Length 168;  
Best Local Similarity 63.9%; Pred. No. 8.2e-34;  
Matches 99; Conservative 16; Mismatches 32; Indels 8; Gaps 2;  
  
QY 9 MEPSADWLATAAARGVEEVRALLEAVLPNAPNSYGRRPQVMMGMSARVAELLLHGA 68  
DB 1 MESAADRLARAAGRVHDVHVRALLEAGVSPNAPNSGRTPIQVMMGNVHVAALLNYGA 60  
  
QY 69 EPNCADPATLTRPVHDAAREGFDTLVVLRACARLDVDRDAGRLPVDLAELGHRDVAR 128  
DB 61 DSNCEDPTTFSRPVHDAAREGFDTLVVLRGSGARLDVDRDAGRLPLDLAQRGHQDIVR 120  
  
QY 129 YLRAA-----AGGT--RGSNHARIDAAEGPSDIP 155  
DB 121 YLRSGCGLSCAGWSLCTAGNVAQTGDGHSFSSSTP 155  
  
RESULT 5  
O89088 PRELIMINARY; PRT; 168 AA.  
O89088;  
DT 01-NOV-1998 (TREMBLrel. 08, Created)  
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE CYCLIN DEPENDENT KINASE INHIBITOR P16INK4A (P16INK4A TUMOR SUPPRESSOR  
PROTEIN) (CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN).  
GN CDKN2A OR E1ALPHA OR P16.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/CANPT; TISSUE=SPLEEN;  
RX MEDLINE=98151529; PubMed=9482902;  
RA Zhang S., Ramsay E.S., Mock B.A.;  
RT "Cdkn2a, the cyclin-dependent kinase inhibitor encoding p16INK4a and  
p19ARF, is a candidate for the plasmacytoma susceptibility locus,  
Pctrl.1";  
RL Proc. Natl. Acad. Sci. U.S.A. 95:2429-2434(1998).  
RN [2]  
RP SEQUENCE OF 1-42 FROM N.A.  
RC STRAIN=MA/MAJ;  
RX MEDLINE=97179476; PubMed=9021155;
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RA Herzog C.R., You M.;  
RT "Sequence variation and chromosomal mapping of the murine Cdkn2a tumor  
suppressor gene.";  
RL Mamm. Genome 8:65-66(1997).  
RN [3]  
RP SEQUENCE OF 1-42 FROM N.A.  
RC STRAIN=BALB/CJ AND MUS POSCHIAVINUS;  
RA Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M.,  
RA Pellicer A., Fernandez-Piqueras J.;  
RT "Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences  
in mouse inbred strains";  
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF044335; AAC08962.1; -  
DR EMBL; U49279; AAC00051.1; -  
DR EMBL; U79626; AAD00224.1; -  
DR HSSP; P55273; 1BD8.  
MGD; MGI:104738; Cdkn2a.  
InterPro: IPR002110; -  
DR Pfam; PF00023; ank; 4.  
DR PROSITE; PS50297; ANK_REP_REGION; 1.  
DR SMART; SM00248; ANK; 1.  
KW Kinase; Cyclin.  
SQ SEQUENCE 168 AA; 17915 MW; 356A973BEAC4D167 CRC64;  
  
Query Match 59.2%; Score 474; DB 11; Length 168;  
Best Local Similarity 63.2%; Pred. No. 1.2e-33;  
Matches 98; Conservative 17; Mismatches 32; Indels 8; Gaps 2;  
  
QY 9 MEPSADWLATAAARGVEEVRALLEAVLPNAPNSYGRRPQVMMGMSARVAELLLHGA 68  
DB 1 MESAADRLARAAGRVHDVHVRALLEAGVSPNAPNSGRTPIQVMMGNVHVAALLNYGA 60  
  
QY 69 EPNCADPATLTRPVHDAAREGFDTLVVLRACARLDVDRDAGRLPVDLAELGHRDVAR 128  
DB 61 DSNCEDPTTFSRPVHDAAREGFDTLVVLRGSGARLDVDRDAGRLPLDLAQRGHQDIVR 120  
  
QY 129 YLRAA-----AGGT--RGSNHARIDAAEGPSDIP 155  
DB 121 YLRSGCGLSCAGWSLCTAGNVAQTGDGHSFSSSTP 155  
  
RESULT 6  
O89088 PRELIMINARY; PRT; 102 AA.  
O89088;  
DT 01-NOV-1999 (TREMBLrel. 12, Created)  
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE P16/CDKN2A/MTS1 (FRAGMENT).  
OS Felis silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
OX NCBI_TaxID=9685;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PBMC;  
RA Okuda M., Cho K., Setoguchi A., Minehata K., Yazawa M., Endo Y.,  
RA Nishigaki K., Watari T., Tsujimoto H., Hasegawa A.;  
RT "Cloning and chromosomal mapping of the feline genes p16(MTS1/CDKN2A),  
and p15(MTS2/CDKN2B).";  
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB010807; BAA33540.1; -  
DR HSSP; P42771; 1BI7.  
MGD; MGI:104738; Cdkn2a.  
InterPro: IPR002110; -  
DR Pfam; PF00023; ank; 3.  
DR PROSITE; PS50297; ANK_REP_REGION; 1.  
FT NON_TER 102  
SQ SEQUENCE 102 AA; 10824 MW; 26399FF21359F35D CRC64;
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Query Match 56.1%; Score 449; DB 6; Length 102;

RN	[1]	SEQUENCE FROM N.A.
RP		TISSUE=PBMC;
RC		

DE CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT) .  
GN P15.

OS	Mus spretus (Western wild mouse).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX	NCBI_TaxID=10096;
[1]	
RN	SEQUENCE FROM N.A.
RP	STRAIN=SPRET/EI.
RC	Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M.,
RA	Pellicer A., Fernandez-Piqueras J.;
RA	"Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
RT	in mouse inbred strains.";
RL	Submitted (OCT-1996) to the EMBL/Genbank/DBJ databases.
DR	EMBL; U79637; AAC00237.1; -.
DR	HSSP; P55273; 1BD8.
DR	InterPro; IPR002110; -.
DR	PROSITE; PS50297; ANK_REP_REGION; 1.
KW	Kinase; Cyclin.
FT	NON_TER 1
FT	NON_TER 86
FT	SEQUENCE 86 AA: 9269 MW; 509D9B3613251B18 CRC64;
Query Match	51.0%; Score 408; DB 11; Length 86;
Best Local Similarity	92.9%; Pred.No. 2.7e-28;
Matches	79; Conservative 2; Mismatches 4; Indels 0; Gaps
QY	51 VMMGMSARVAELLHGAEPNCADPATLTLPVHDAAREGLDTLVVLRAGARDVDWA 110       
Dd	1 VMMGSAQVAELLHGAEPNCADPATLTLPVHDAAREGLDTLVVLRAGARDVDCA 60       
QY	111 GRIPVDLAEEIGHRDVARYLRAAG 135       
Dd	61 GRIPVDLAEEQGHRDIARYLHAATG 85       

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RESULT 11
Q90UP0 PRELIMINARY; PRT;      86 AA.
AC Q90P0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT).
GN p15.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OC NCBI_TaxID=10090;
OY [1]
SEQUENCE FROM N.A.
RC STRAIN-VARIOUS STRAINS;
RA Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M.,
RA Pellicer A., Fernandez-Piqueras J.;
RT "Comparative analysis of the pl6(INK4a) and pl5(INK4b) DNA sequences
in mouse inbred strains.";
RL Submitted (Oct-1996) to the EMBL/GenBank/DDJB databases.
DR EMBL; U79639; AAD00234.1; -.
DR EMBL; U79636; AAD00232.1; -.
DR EMBL; U79638; AAD00233.1; -.
DR InterPro; IPR002110; -.
DR PROSITE; PS50297; ANK_REP_REGION; 1.
KW Kinase; Cyclin.
FT NON_TER 1
FT NON_TER 86
SQ SEQUENCE      86 AA;  9269 MW;  509D9B3613251B18 CRC64;

Query Match          51.0%; Score 408; DB 11; Length 86;
Best Local Similarity 92.9%; Pred. No. 2.7e-28;
Matches 79; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 51 VMVMGSGARVAELLHLHGAEPCNCPADPTLRPVHDAAREGFLDTLVVLRAGARLDVRDAW 110
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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Db      1  VMMGSGQAPELLLLHGAEPNCADPAITLTPVPVHDAAREGFIDTLVLVHHRAGARLDVCDAW 60
Qy      11 1  GRLPVDLAAEELGHRDVARYLRAAAG 135
          |||||  |||||  |||||  ||  |
Db      61  GRLPVDLAAEQGHRDIARYLHAATG 85

RESULT 12
Q9TSY0  PRELIMINARY;          PRT;      86 AA.
AC      Q9TSY0;
DT      01-MAY-2000 (TrEMBLrel. 13, Created)
DT      01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT      01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE      CYCLIN-DEPENDENT KINASE INHIBITOR P15 (FRAGMENT).
GN      CDKN2B.
OS      Sus scrofa (Pig).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX      Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OC      NCBI_TaxID=9823;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=LARGE WHITE;
RA      Le Chalony C., Hayes H., Frelat G., Gefirofin C.;
RT      "Identification and mapping of swine CDKN2A and CDKN2B exon2
RT      sequences."
RL      Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AJ242788; CAB65455.1; -.
DR      HSP; P55273; IBD8.
DR      InterPro; IPR002110; -.
DR      Pfam; PF00023; ank; 2.
DR      PROSITE; PS50297; ANK_REP_REGION; 1.
KW      Kinase; Cyclin.
SQ      NON_TER 1
SQ      SEQUENCE 86 AA; 9286 MW; 16EF7A232393GCF9 CRC64;

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Query Match	50.9%;	Score 407;	DB 6;	Length 86;
Best Local Similarity	92.9%;	Pred. No. 3.3e-28;		
Matches	79;	Conservative 3;	Mismatches 3;	Indels 0; Gaps
Qy	51	VMMGSRVAEELLLLHGAENPCADPATLT	RPVHDAAREGFLDTLV	LHRRAGARLDDVRDAW 110
Db	1	VMMGSRVAEELLLLHGAENPCADPATLT	RPVHDAAREGFLDTLV	LRRAGARLDDVQDAW 60
Qy	111	GRLPVDLAEEELGHRDVARYLRAAG	135	
Db	61	GRLPVDLAEEERHRDVARYLRAAG	85	

RESULT	13
O54846	
ID	054846 PRELIMINARY; PRT; 86 AA.
AC	C54846;
DT	01-JUN-1998 (TrEMBLrel. 06, Created)
DT	01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DE	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE	CYCLIN-DEPENDENT KINASE INHIBITOR P15INK4B (FRAGMENT).
GN	CDKN2B.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
NCBI_TaxID=10090;	
[1]	
RN	
SEQUENCE FROM N.A.	
RC	STRAIN=C57BL/6J;
RA	Malumbres M., Pellicer A.;
RL	Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AF015460; AAB94534.1; "
DR	HSSP; P55273; 1BD8.
DR	InterPro; IPR002110; "
DR	PROSITE; PS50297; ANK_REP_REGION; 1.
FT	NON TER 1

Search completed: October 31, 2001, 07:13:46  
Job time: 538 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 31, 2001, 07:02:33 ; Search time 51.96 Seconds  
(without alignments)  
182.012 Million cell updates/sec

Title: US-09-016-869A-2  
Perfect score: 800  
Sequence: 1 MDPAGSMPEPSDWLATAA.....TRGSNHARIDAEGPSDIPD 156

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues  
1 number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :				A_Geneseq_0601.*
1:	/SID88/gcgdata/geneseq/geneseq/AA1980.DAT.*			
2:	/SID88/gcgdata/geneseq/geneseq/AA1981.DAT.*			
3:	/SID88/gcgdata/geneseq/geneseq/AA1982.DAT.*			
4:	/SID88/gcgdata/geneseq/geneseq/AA1983.DAT.*			
5:	/SID88/gcgdata/geneseq/geneseq/AA1984.DAT.*			
6:	/SID88/gcgdata/geneseq/geneseq/AA1985.DAT.*			
7:	/SID88/gcgdata/geneseq/geneseq/AA1986.DAT.*			
8:	/SID88/gcgdata/geneseq/geneseq/AA1987.DAT.*			
9:	/SID88/gcgdata/geneseq/geneseq/AA1988.DAT.*			
10:	/SID88/gcgdata/geneseq/geneseq/AA1989.DAT.*			
11:	/SID88/gcgdata/geneseq/geneseq/AA1990.DAT.*			
12:	/SID88/gcgdata/geneseq/geneseq/AA1991.DAT.*			
13:	/SID88/gcgdata/geneseq/geneseq/AA1992.DAT.*			
14:	/SID88/gcgdata/geneseq/geneseq/AA1993.DAT.*			
15:	/SID88/gcgdata/geneseq/geneseq/AA1994.DAT.*			
16:	/SID88/gcgdata/geneseq/geneseq/AA1995.DAT.*			
17:	/SID88/gcgdata/geneseq/geneseq/AA1996.DAT.*			
18:	/SID88/gcgdata/geneseq/geneseq/AA1997.DAT.*			
19:	/SID88/gcgdata/geneseq/geneseq/AA1998.DAT.*			
20:	/SID88/gcgdata/geneseq/geneseq/AA1999.DAT.*			
21:	/SID88/gcgdata/geneseq/geneseq/AA2000.DAT.*			
22:	/SID88/gcgdata/geneseq/geneseq/AA2001.DAT.*			

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	800	100.0	156	AAR85116	Cell-cycle regulat
2	800	100.0	156	20 AAY24741	Human INK-4 protei
3	800	100.0	156	21 AAY88354	Human cell cycle r
4	789	98.6	156	18 AAW10627	Tumour suppressor
5	789	98.6	156	18 AAW19251	Human multiple tum
6	789	98.6	156	19 AAW74549	Amino acid sequenc
7	789	98.6	156	19 AAW40524	Human MTS1 protein
8	789	98.6	156	20 AAW80524	A human multiple t
9	789	98.6	156	21 AAB15498	Human MTS1 protein
10	789	98.6	156	21 AAY97524	Human p16 protein
11	789	98.6	156	21 AAY96053	Human cyclin depen

12	789	98.6	156	21	AAY96067	Human cyclin depen
13	789	98.6	156	21	AAY92921	Human multiple tum
14	789	98.6	156	21	AAY91102	Human multiple tum
15	789	98.6	156	21	AAY59415	Human MTS1 protein
16	789	98.6	156	21	AAY54902	Human multiple tum
17	789	98.6	156	22	AAB67334	Protein encoded by
18	789	98.6	156	22	AAB36890	Human Multiple Tum
19	788	98.5	228	21	AAY97522	Human W9 protein s
20	788	98.5	228	21	AAY96051	Antiproliferative
21	788	98.5	228	21	AAY96078	Angiogenesis inhib
22	788	98.5	237	20	AAW95105	Truncated p27/p16
23	788	98.5	237	21	AAY97534	Human W9 protein s
24	788	98.5	237	21	AAY96049	Antiproliferative
25	788	98.5	237	21	AAY96076	Angiogenesis inhib
26	788	98.5	252	20	AAW95106	Truncated p27/p16
27	788	98.5	252	21	AAY97535	Human W10 protein
28	788	98.5	252	21	AAY96050	Antiproliferative
29	788	98.5	323	21	AAY96079	Angiogenesis inhib
30	788	98.5	323	21	AAW95103	Secretable angio
31	788	98.5	334	20	AAW95107	Truncated p27/p16
32	788	98.5	334	21	AAY97532	Human W8 protein s
33	788	98.5	334	21	AAY96047	Antiproliferative
34	788	98.5	334	21	AAY96074	Angiogenesis inhib
35	788	98.5	365	18	AAW23536	CDK inhibitory fus
36	788	98.5	365	20	AAW95107	Human p16p27 fusio
37	788	98.5	365	20	AAW95096	Human p16p27 fusio
38	788	98.5	365	21	AAY97527	Human W4 protein s
39	788	98.5	365	21	AAY97529	Human W6 protein s
40	788	98.5	365	21	AAY96042	Antiproliferative
41	788	98.5	365	21	AAY96044	Antiproliferative
42	788	98.5	365	21	AAY96069	Angiogenesis inhib
43	788	98.5	365	21	AAY96071	Angiogenesis inhib
44	788	98.5	380	18	AAW23535	CDK inhibitory fus-
45	788	98.5	380	20	AAW95095	Human p16(GS)p27 f

ALIGNMENTS

RESULT 1	
AAR85116	
ID	AAR85116 standard; Protein; 156 AA.
XX	
AC	AAR85116;
XX	
DT	01-MAR-1996 (first entry)
XX	
DE	Cell-cycle regulatory protein p16.
XX	
KW	Cell-cycle regulatory protein p16; cyclin-dependent kinase inhibitor;
KW	CCR; cancer; cell proliferation.
XX	
OS	Homo sapiens.
XX	
PN	W09528483-A1.
XX	
PD	26-OCT-1995.
XX	
PF	14-APR-1995; 95WO-US04636.
XX	
PR	29-NOV-1994; 94US-0346147.
PR	14-APR-1994; 94US-0227371.
PR	25-MAY-1994; 94US-0248812.
PR	14-SEP-1994; 94US-0306511.
XX	
PA	(COLD-) COLD SPRING HARBOR LAB.
XX	
PI	Beach DH, Demetrick DJ, Hannon GJ, Serrano M;
XX	
DR	WPI; 1995-373798/48.
DR	N-PSDB; AAT02962.
XX	
PT	New cell cycle regulating proteins bind to cyclin dependent kinase -



PT disorder characterized by unwanted cell proliferation or  
XX differentiation -  
PS Claim 14; Column 57-58; 61pp; English.  
XX  
CC This sequence represents the human cell cycle regulatory protein (CCR)  
CC p16 amino acid sequence. The p16 gene is located on chromosome 9p21-22.  
CC The invention relates to a diagnostic assay which comprises detecting a  
CC mutation in the p16 gene, which is used to identify a cell or cells at  
CC risk of developing a disorder characterized by unwanted cell  
CC proliferation or differentiation. p16 is a cyclin-dependent kinase  
CC (CDK)-inhibitory protein, and functions as an inhibitor of cell-cycle  
CC progression and ultimately cell growth. The assay can be used for  
CC identifying a cell or cells at risk for a disorder (neoplasia)  
CC characterized by unwanted cell proliferation or differentiation. The  
CC method is used for detecting mutations in either a CCR gene or CDK gene  
CC which alter complex formation between these two proteins. The method is  
CC also used for detecting mutations in other cellular proteins which  
CC disrupt protein interactions such as mutations which disrupt binding of  
CC the p53 protein with other cellular proteins, e.g. Wilm's tumour  
CC suppressor protein Wt1. They can also be used to detect mutations in  
CC pairs of signal transduction proteins such as ras protein or other  
CC cellular proteins which interact with ras, e.g. ras GTPase activating  
CC proteins (GAPs). The method is convenient for detecting mutants of CCR  
CC genes encoding proteins which are unable to physically interact with a  
CC CDK bait protein.  
XX  
SQ Sequence 156 AA;

Query Match 100.0%; Score 800; DB 21; Length 156;  
Best Local Similarity 100.0%; Pred. No. 4.6e-86;  
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MDPAGSSMEPSADWLATAAARGVEEVRLLEVALPNAPNSYGRPIQVMMGSAVA 60  
DB 1 mdpagssmepeadwlataaargveevrlllevalpnapsygrpiqvmmgmsarva 60  
QY 61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAE 120  
DB 61 elllllhgaepncadpatltrpvhdaaregfldtlvvlhragarlvdvdawgrlpvdlae 120  
QY 121 LGRDVARVYLRAGAGTGRGSHARIDAEGPSDIPD 156  
DB 121 lgrdvarylraaaggrtgrsharidaaegpsdipd 156

RESULT 4  
AAW10627  
AAW10627 standard; Protein; 156 AA.  
XX  
AC AAW10627;  
XX  
DT 28-OCT-1997 (first entry)  
XX  
DE Tumour suppressor p16.  
XX  
KW Tumour suppressor; p16; inhibitor; cyclin-dependent kinase 4; CDK4;  
KW cancer cell; lung cancer; bladder cancer; melanoma; restenosis; therapy;  
KW anti-angiogenic activity; hyperproliferative disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO9703635-A2.  
XX  
PD 06-FEB-1997.  
XX  
PF 17-JUL-1996; 96WO-US11787.  
XX  
PR 17-JUL-1995; 95US-0502881.  
XX  
PA (TEXA ) UNIV TEXAS SYSTEM.  
XX

PI Jin X, Roth J;  
XX WPI; 1997-132336/12.  
DR N-PSDB; AAT60951.  
XX  
PT Expression construct contg. DNA for tumour suppressor p16 - to  
PT restore p16 activity to transformed cells, useful for treating lung  
PT or bladder cancer or melanoma  
XX  
PS Disclosure; Fig 1b; 92pp; English.  
XX  
CC This sequence represents the tumour suppressor p16. The DNA encoding  
CC this sequence is joined to a promoter functional in eukaryotic cells and  
CC used in the expression construct of the invention. p16 is an inhibitory  
CC subunit, which is involved in the control of cyclin-dependent kinase 4  
CC activity, and functions as a tumour suppressor. By detecting this  
CC sequence or the DNA encoding it, cancer cells can be detected. When the  
CC nucleic acid molecule is in the sense orientation, the expression  
CC construct can be used to restore p16 function in a cell, particularly by  
CC reversing the transformed phenotype in tumours, especially lung or  
CC bladder cancer or melanoma. It may also have anti-angiogenic activity,  
CC and inhibit hyperproliferative disorders, e.g. restenosis. When the  
CC nucleic acid molecule is inserted in the antisense orientation, the  
CC expression construct inhibits p16 function. Reduced or increased levels  
CC of p16, or a related nucleic acid, may be diagnostic of tumours, e.g. by  
CC Southern or Northern blot, antibody immunoblot, fluorescent cell sorting  
CC or immunoassay.  
XX  
SQ Sequence 156 AA;

Query Match 98.6%; Score 789; DB 18; Length 156;  
Best Local Similarity 98.7%; Pred. No. 8.9e-85;  
Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MDPAGSSMEPSADWLATAAARGVEEVRLLEVALPNAPNSYGRPIQVMMGSAVA 60  
DB 1 mdpagssmepeadwlataaargveevrlllevalpnapsygrpiqvmmgmsarva 60  
QY 61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAE 120  
DB 61 elllllhgaepncadpatltrpvhdaaregfldtlvvlhragarlvdvdawgrlpvdlae 120  
QY 121 LGRDVARVYLRAGAGTGRGSHARIDAEGPSDIPD 156  
DB 121 lgrdvarylraaaggrtgrsharidaaegpsdipd 156

RESULT 5  
AAW19251  
ID AAW19251 standard; Protein; 156 AA.  
XX  
AC AAW19251;  
XX  
DT 10-SEP-1997 (first entry)  
XX  
DE Human multiple tumour suppressor 1 gene product.  
XX  
KW Human; multiple; tumour; suppressor; MTS1; cancer; diagnosis.  
XX  
OS Homo sapiens.  
XX  
PN US5624819-A.  
XX  
PD 29-APR-1997.  
XX  
PF 18-MAR-1994; 94US-0214582.  
XX  
PR 07-JUN-1995; 95US-0474177.  
PR 18-MAR-1994; 94US-0214582.  
PR 18-MAR-1994; 94US-0215086.  
PR 18-MAR-1994; 94US-0215087.  
PR 14-APR-1994; 94US-0227369.  
XX

PR 01-JUN-1994; 94US-0251938.  
PR 17-MAR-1995; 95WO-US03537.  
XX (MYRI-) MYRIAD GENETICS INC.  
PA (UTAH ) UNIV UTAH RES FOUND.  
XX Cannon-Albright LA, Kamb A, Skolnick MH;  
PI WPI; 1997-258217/23.  
DR N-PSDB; AAT72311.  
XX Human mutant multiple tumour suppressor gene sequences - for  
PT production of recombinant mutant polypeptide(s)  
XX Claim 1; Columns 61-64; 72pp; English.  
PS The present sequence the human multiple tumour suppressor 1  
CC (MTS1) gene product, useful in cancer diagnosis.  
XX Sequence 156 AA;  
Query Match 98.6%; Score 789; DB 18; Length 156;  
Best Local Similarity 98.7%; Pred. No. 8.9e-85;  
Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MDPAGSSMEPSADWLATAAARGVEEVRLLEAVALPNAPNSYGRRIQVMMGSAARVA 60  
Db 1 mepaagssmepsadwlataaaargveevrllleagalpnapnsygrriqvmmgsarva 60  
QY 61 ELLLLHGAEPNCADPATLTRPVHDAAREGFDTLVVLRHAGARLDVDRDAGRLPVDLAE 120  
Db 61 ellllhgaepncadpatltrpvhdaaregfdtlvvllhragarldvdrdawgrlpvdlae 120  
QY 121 LGHRDVARYLRAAAGTGRGSHARIDAAEGPSDIPD 156  
Db 121 lghrdvarylraaagtgrgsharidaaegpsdipd 156  
RESULT 6  
AAW74549  
ID AAW74549 standard; Protein; 156 AA.  
XX AC AAW74549;  
XX DT 04-DEC-1998 (first entry)  
XX Amino acid sequence of multiple tumour suppressor 1.  
XX Multiple tumour suppressor 1; MTS-1; human; cancer; hybridisation;  
KW somatic mutation; gene therapy.  
XX Homo sapiens.  
XX US5801236-A.  
XX PD 01-SEP-1998.  
XX PF 07-JUN-1995; 95US-0480810.  
XX PR 07-JUN-1995; 95US-0480810.  
XX PR 18-MAR-1994; 94US-0214582.  
XX PR 18-MAR-1994; 94US-0215086.  
XX PR 18-MAR-1994; 94US-0215087.  
XX PR 14-APR-1994; 94US-0227369.  
XX PR 01-JUN-1994; 94US-0251938.  
XX PR 17-MAR-1995; 95WO-US03316.  
XX (MYRI-) MYRIAD GENETICS INC.  
XX Kamb A;  
XX WPI; 1998-494842/42.

DR N-PSDB; AAV53819.  
XX Nucleic acids based on multiple tumour suppressor, MTS, sequences -  
PT useful as hybridisation probes, primers and recombinant production  
PT of MTS in the diagnosis and treatment of cancers related to MTS  
PT mutation(s)  
XX Disclosure; Column 63-64; 73pp; English.  
PS This is the amino acid sequence of the multiple tumour suppressor 1  
CC (MTS-1) protein, used in the method of the invention. The MTS gene  
CC is useful in the diagnosis and prognosis of human cancer, e.g. by  
CC standard nucleic hybridisation techniques, of patient samples. The  
CC mutated sequences are those that are present in somatic mutations  
CC of the gene in cancers. The vectors can be used for gene therapy  
CC strategies to replace function of mutated protein in patients. These  
CC can also be used to construct protein mimetics, also for therapeutic  
CC strategies. In addition the expression constructs can also be used  
CC for recombinant production of MTS. Recombinant MTS can be used to  
CC screen for drugs to be used for cancer therapy, and the protein  
CC itself may also be used to restore MTS function in a cell.  
XX Sequence 156 AA;  
SQ Query Match 98.6%; Score 789; DB 19; Length 156;  
Best Local Similarity 98.7%; Pred. No. 8.9e-85;  
Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MDPAGSSMEPSADWLATAAARGVEEVRLLEAVALPNAPNSYGRRIQVMMGSAARVA 60  
Db 1 mepaagssmepsadwlataaaargveevrllleagalpnapnsygrriqvmmgsarva 60  
QY 61 ELLLLHGAEPNCADPATLTRPVHDAAREGFDTLVVLRHAGARLDVDRDAGRLPVDLAE 120  
Db 61 ellllhgaepncadpatltrpvhdaaregfdtlvvllhragarldvdrdawgrlpvdlae 120  
QY 121 LGHRDVARYLRAAAGTGRGSHARIDAAEGPSDIPD 156  
Db 121 lghrdvarylraaagtgrgsharidaaegpsdipd 156  
RESULT 7  
AAW40524  
ID AAW40524 standard; Protein; 156 AA.  
XX AC AAW40524;  
XX DT 15-JUL-1998 (first entry)  
XX Human Mts1 protein.  
XX MTS1; multiple tumour suppressor; diagnosis; cancer; germ-line mutation;  
KW familial melanoma locus; MLM; predisposition.  
XX Homo sapiens.  
XX US5739027-A.  
XX PD 14-APR-1998.  
XX PF 07-JUN-1995; 95US-0487033.  
XX PR 07-JUN-1995; 95US-0487033.  
XX PR 18-MAR-1994; 94US-0214582.  
XX PR 18-MAR-1994; 94US-0215086.  
XX PR 18-MAR-1994; 94US-0215087.  
XX PR 14-APR-1994; 94US-0227369.  
XX PR 01-JUN-1994; 94US-0251938.  
XX PR 17-MAR-1995; 95WO-US03316.  
XX (MYRI-) MYRIAD GENETICS INC.  
XX PA



PI Kamb A;  
 XX WPI; 1998-250421/22.  
 DR N-PSDB; AAV11238.  
 XX  
 PT DNA specific for Multiple Tumour Suppressor 1E1-beta gene - are  
 PT useful for the diagnosis of cancers related to MTS1E1-beta  
 PT mutation(s) and their treatment  
 XX  
 PS Disclosure; Column 63-64; 72pp; English.  
 XX  
 CC This sequence represents a human multiple tumour suppression protein,  
 CC MTS1. The MTS gene locus is also referred to as the familial melanoma  
 CC (MLM) gene locus, located on human chromosome 9p21. Germ line mutations  
 CC in MTS genes can be used in the diagnosis of predisposition to cancers,  
 CC e.g. melanoma, leukaemia, astrocytoma, glioblastoma, lymphoma, glioma,  
 CC Hodgkin's lymphoma, CLL, and cancers of the pancreas, breast, thyroid,  
 CC ovary, uterus, testis, kidney, stomach and rectum.  
 XX  
 XX Sequence 156 AA;  
 Query Match 98.6%; Score 789; DB 19; Length 156;  
 Best Local Similarity 98.7%; Pred. No. 8.9e-85;  
 Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MDPAGSSMEPSADWLATAAARGVEEVRALEAVALPNAPNSYGRRPQVMMGSGARVA 60  
 Db 1 mepaagssmepsadwlataaargveevraalleagalpnapnsygrripqvmmgsgarva 60  
 QY 61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAE 120  
 Db 61 e111llhgaepncadpatltrpvhdaaregfdltlvvlhragardlvrddawgripvdlae 120  
 QY 121 LGRDVARYLRAAAGGTRGSHARIDAAEGPSDIPD 156  
 Db 121 lghrdvarylraaaggtrgsharidaaegpsdipd 156  
 RESULT 8  
 AAW80524  
 ID AAW80524 standard; Protein; 156 AA.  
 AC AAW80524;  
 XX  
 XX 03-FEB-1999 (first entry)  
 DT  
 DE A human multiple tumour suppressor 1 (MTS1) protein.  
 DR Human; multiple tumour suppressor 1 gene; MTS1; cancer.  
 XX Homo sapiens.  
 OS  
 XX US5843756-A.  
 PN  
 XX 01-DEC-1998.  
 PD  
 XX 28-JUL-1995; 95WO-0508735.  
 PF  
 XX 28-JUL-1995; 95US-0508735.  
 PR  
 XX 07-JUN-1995; 95US-0487033.  
 XX (MYRI-) MYRIAD GENETICS INC.  
 PA Jiang P, Kamb A, Stone S;  
 XX  
 PI WPI; 1999-044585/04.  
 DR N-PSDB; AAV70583.  
 XX  
 XX Mouse multiple tumour suppressor gene segment - useful for primer  
 design  
 PT  
 XX Disclosure; Columns 65-66; 80pp; English.  
 PS

XX The present sequence represents a human multiple tumour suppressor 1  
 CC (MTS1) protein. The sequence is homologous to the corresponding  
 CC murine gene. Primers designed from the gene can be used to design  
 CC primers to detect abnormalities i.e. polymorphisms which may  
 CC predispose towards malignancies such as melanoma, leukaemia,  
 CC astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast,  
 CC thyroid, pancreas, uterus and kidneys.  
 XX  
 XX Sequence 156 AA;  
 Query Match 98.6%; Score 789; DB 20; Length 156;  
 Best Local Similarity 98.7%; Pred. No. 8.9e-85;  
 Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MDPAGSSMEPSADWLATAAARGVEEVRALEAVALPNAPNSYGRRPQVMMGSGARVA 60  
 Db 1 mepaagssmepsadwlataaargveevraalleagalpnapnsygrripqvmmgsgarva 60  
 QY 61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAE 120  
 Db 61 e111llhgaepncadpatltrpvhdaaregfdltlvvlhragardlvrddawgripvdlae 120  
 QY 121 LGRDVARYLRAAAGGTRGSHARIDAAEGPSDIPD 156  
 Db 121 lghrdvarylraaaggtrgsharidaaegpsdipd 156  
 RESULT 9  
 AAB15498  
 ID AAB15498 standard; Protein; 156 AA.  
 XX  
 AC AAB15498;  
 XX  
 XX 14-FEB-2001 (first entry)  
 DT  
 DE Human MTS1 protein.  
 XX Cytostatic; human; multiple tumour suppressor 1; MTS1; diagnostic;  
 KW cancer; gene therapy; protein replacement therapy.  
 XX Homo sapiens.  
 OS  
 XX US6090578-A.  
 PN  
 XX 18-JUL-2000.  
 PD  
 XX 08-DEC-1997; 97US-0986515.  
 PF  
 XX 07-JUN-1995; 95US-0480810.  
 PR  
 XX 18-MAR-1994; 94US-0214582.  
 PR  
 XX 18-MAR-1994; 94US-0215086.  
 PR  
 XX 18-MAR-1994; 94US-0215087.  
 PR  
 XX 01-JUN-1994; 94US-0227369.  
 PR  
 XX 01-JUN-1994; 94US-0251938.  
 PR  
 XX 17-MAR-1995; 95WO-US03316.  
 XX (MYRI-) MYRIAD GENETICS INC.  
 PA Kamb A;  
 XX  
 PI WPI; 2000-514036/46.  
 DR N-PSDB; AAA95633.  
 XX  
 XX Novel protein composition useful in protein replacement therapy for  
 PT diagnosing and treating cancer comprises a specific weight percent of  
 PT human multiple tumour suppressor 1 polypeptide -  
 XX  
 XX Claim 4; Column 63-64; 72pp; English.  
 PS  
 XX This sequence represents the human multiple tumour suppressor 1 (MTS1)  
 CC amino acid sequence. The protein has a cytostatic activity and is used in

CC protein replacement therapy. WTS1 is useful in diagnosing human cancers  
CC such as (ocular) melanoma, leukemia, astrocytoma, glioblastoma, lymphoma,  
CC glioma, Hodgkin's lymphoma, multiple myeloma, sarcoma, myosarcoma,  
CC cholangiocarcinoma, squamous cell carcinoma, CLL, and cancers of  
CC pancreas, breast, stomach, brain, prostate, bladder, thyroid, ovary,  
CC uterus, testis, kidney, colon and rectum. The WTS1 gene and protein is  
CC useful in gene therapy, protein replacement therapy and protein mimetic  
CC studies.

XX Sequence 156 AA;

Query Match 98.6%; Score 789; DB 21; Length 156;  
Best Local Similarity 98.7%; Pred. No. 8.9e-85;  
Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDPAGSSMEPSADWLATAAARGVEEVRLLEAVLPNAPNSYGRPRPQVMMGMSARVA 60

Db 1 mepaagssmepsadwlataaargveevrllleagalpnapnsygrprpqvmmgmsarva 60

61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAE 120

Db 61 ellllhgaepncadpatltrpvhdaaregfltdlvvlhragarldvrdawgripvdlae 120

QY 121 LGRDVARYLRAAAGTGRGSHARIDAEGPSDIPD 156

Db 121 lgrdvarylraaagtrgsharidaaegpsdipd 156

RESULT 10

AA97524

ID AA97524 standard; Protein; 156 AA.

XX AC AA97524;

XX 15-JAN-2001 (first entry)

DE Human p16 protein sequence.

KW Human; chimeric cyclin dependent kinase inhibitor; CDK1; therapy;  
KW adenovirus E4 protein; neoplasia; p16 protein.

XX OS Homo sapiens.

XX WO200052184-A1.

XX 08-SEP-2000.

01-MAR-2000; 2000WO-US05350.

01-MAR-1999; 99US-0122974.

08-APR-1999; 99US-0128271.

09-APR-1999; 99US-0128515.

XX (CELL-) CELL GENESYS INC.

PA (MITO-) MITOTIX INC.

PI Patel S, McArthur J, Gyuris J, Mendez MJ, Finer M;

XX WPI; 2000-587315/55.

DR N-PSDB; AAA90921.

PT Protein and nucleic acid compositions for preventing and treating  
PT neoplasias (particularly cancer), comprises a novel chimeric cyclin  
PT dependent kinase inhibitor and adenovirus E4 protein -

XX Example 1; Page 123; 126pp; English.

XX This sequence represents the human p16 protein.

CC The invention relates to a protein composition comprising a novel

CC purified chimeric cyclin dependent kinase inhibitor (CDK1) and a  
CC purified adenovirus E4 protein. The compositions comprising the protein,  
CC or the DNA encoding it are useful for treating neoplasias in animals. The

CC compositions also find use in assays to eliminate a specific  
CC sub-population of cultured cells, to determine the susceptibility of  
CC neoplastic cells to treatment with the compositions and also in assays to  
CC synchronise cell growth in cultured cells.

XX Sequence 156 AA;

Query Match 98.6%; Score 789; DB 21; Length 156;  
Best Local Similarity 98.7%; Pred. No. 8.9e-85;  
Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDPAGSSMEPSADWLATAAARGVEEVRLLEAVLPNAPNSYGRPRPQVMMGMSARVA 60

Db 1 mepaagssmepsadwlataaargveevrllleagalpnapnsygrprpqvmmgmsarva 60

QY 61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAE 120

Db 61 ellllhgaepncadpatltrpvhdaaregfltdlvvlhragarldvrdawgripvdlae 120

QY 121 LGRDVARYLRAAAGTGRGSHARIDAEGPSDIPD 156

Db 121 lgrdvarylraaagtrgsharidaaegpsdipd 156

RESULT 11

AA96053

ID AA96053 standard; Protein; 156 AA.

XX AC AA96053;

XX 05-DEC-2000 (first entry)

DE Human cyclin dependent kinase inhibitor p16.

XX Cyclin dependent kinase inhibitor; CDK1; human; p16;  
KW smooth muscle cell; restenosis; vasotropic; antiproliferative;  
KW gene therapy.

XX OS Homo sapiens.

XX WO200052159-A1.

XX 08-SEP-2000.

28-FEB-2000; 2000WO-US04971.

01-MAR-1999; 99US-0122974.

05-NOV-1999; 99US-0163682.

09-DEC-1999; 99US-0457568.

XX (CELL-) CELL GENESYS INC.

PA (MITO-) MITOTIX INC.

PI McArthur J, Gyuris J, Finer M;

XX WPI; 2000-594183/56.

DR N-PSDB; AAA50500.

XX Novel recombinant lentivirus for inhibiting proliferation of smooth  
PT muscle cells in e.g. restenosis, is replication deficient and comprises  
PT a transgene encoding a cyclin dependent kinase inhibitor -

XX Example 1; Page 121; 126pp; English.

XX The present sequence is that of human p16, a cyclin dependent  
CC kinase inhibitor (CDK1) that inhibits smooth muscle cell  
CC proliferation. A claimed method for inhibiting smooth muscle cell

CC hyperproliferation involves transducing smooth muscle cells with a  
CC replication-deficient recombinant adenovirus that lacks a functional  
CC E1 region and a functional E4 region, and comprises a transgene  
CC encoding a CDK1. The CDK1 is selected from an INK4 family protein  
CC such as human p16, a CIP/KIP family protein such as p27, active

CC fragments of these, or fusion proteins comprising (active fragments  
CC of) an INK4 family protein and a CIP/KIP family protein (see AAY96046  
CC cell hyperproliferation induced by injury caused by angioplasty,  
CC stent placement or vein engraftment. It is useful for treating  
CC vascular pathologies, e.g. restenosis. Also claimed are recombinant  
CC lentiviruses encoding CDKis.  
XX  
SQ Sequence 156 AA;

Query Match 98.6%; Score 789; DB 21; Length 156;  
Best Local Similarity 98.7%; Pred. No. 8.9e-85;  
Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDPAGSMFSDWLTAAARGVEVRALLEVALPNAPNSYGRRPQVMMGSGARVA 60  
I:|||||  
DB 1 mepaagssmepsadwltataaargrveevrallleagalpnapsygrripqymmgsgarva 60  
61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAE 120  
|||||  
61 ellllhgaepncadpatltrpvhdaaregfdltlvvlhragardvrdawgrlpvdlae 120  
|||||  
QY 121 LGHRDVARYLRAAAGTGRGSHARIDAAEGPSDIPD 156  
|||||  
DB 121 lghrdvarylraaagtgrgsharidaaegpsdipd 156

RESULT 12

ID AAY96067  
ID AAY96067 standard; Protein; 156 AA.

AC AAY96067;

XX 05-DEC-2000 (first entry)

XX Human cyclin dependent kinase inhibitor p16.

XX Cyclin dependent kinase inhibitor; CDK1; INK4; human; p16;  
KW angiogenesis; inhibitor; neoplasia; rheumatoid arthritis;  
KW endometriosis; psoriasis; vascular retinopathy; cytostatic;  
KW antiarthritic; antirheumatic; gynaecological; antipsoriatic;  
KW antiproliferative; gene therapy.

OS Homo sapiens.

XX WO200052158-A1.

XX 08-SEP-2000.

XX 28-FEB-2000; 2000WO-US04970.

XX 01-MAR-1999; 99US-0122974.

XX 05-NOV-1999; 99US-0163682.

XX 09-DEC-1999; 99US-0457646.

XX (CELL-) CELL GENESYS INC.

XX (MITO-) MITOTIX INC.

XX Patel S, McArthur J, Gyuris J;

XX WPI; 2000-565501/52.

XX N-PSDB; AAA50520.

XX Inhibiting angiogenesis and treating angiogenesis-associated

XX conditions, e.g. neoplasia, psoriasis by transducing an endothelial

XX cell with a recombinant virus having a transgene encoding a cyclin

XX dependent kinase inhibitor -

XX Example 1; Page 129; 138pp; English.

XX The present sequence is that of human p16, a cyclin dependent

CC method for inhibiting angiogenesis involves transducing an  
CC epithelial cell with a transgene encoding (internalizable,  
CC secretable) CDK1. The delivery system for the transgene may be a  
CC liposome or a recombinant virus. The CDK1 is preferably a protein  
CC of the CIP/KIP family such as p27, a protein of the INK4 family  
CC such as p16, active fragments of these proteins, or a fusion of 2  
CC CDK1 proteins such as p27 and p16 (see AAY96068-80). The method is  
CC useful in treating conditions associated with angiogenesis, e.g.  
CC neoplasia, rheumatoid arthritis, endometriosis, psoriasis and  
CC vascular retinopathy (claimed). Alternatively, the transgene is  
CC delivered to an auxiliary cell, and is expressed by that cell such  
CC that the CDK1 is released into the blood and contacts the target  
CC epithelial cell.  
XX  
SQ Sequence 156 AA;

Query Match 98.6%; Score 789; DB 21; Length 156;  
Best Local Similarity 98.7%; Pred. No. 8.9e-85;  
Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDPAGSMFSDWLTAAARGVEVRALLEVALPNAPNSYGRRPQVMMGSGARVA 60  
I:|||||  
DB 1 mepaagssmepsadwltataaargrveevrallleagalpnapsygrripqymmgsgarva 60  
61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAE 120  
|||||  
61 ellllhgaepncadpatltrpvhdaaregfdltlvvlhragardvrdawgrlpvdlae 120  
|||||  
QY 121 LGHRDVARYLRAAAGTGRGSHARIDAAEGPSDIPD 156  
|||||  
DB 121 lghrdvarylraaagtgrgsharidaaegpsdipd 156

RESULT 13

AAY92921  
ID AAY92921 standard; Protein; 156 AA.

XX AAY92921;

XX 11-OCT-2000 (first entry)

XX Human multiple tumour suppressor 1 protein.

XX Variant; human; multiple tumour suppressor; MTS; mutation; melanoma;  
KW cancer; diagnosis.

XX Homo sapiens.

XX US6037462-A.

XX 14-MAR-2000.

XX 22-JUL-1998; 98US-0120130.

XX 07-JUN-1995; 95US-0480810.

XX 18-MAR-1994; 94US-0214582.

XX 18-MAR-1994; 94US-0215086.

XX 18-MAR-1994; 94US-0215087.

XX 14-APR-1994; 94US-0227369.

XX 01-JUN-1994; 94US-0251938.

XX 17-MAR-1995; 95WO-US03316.

XX (MYRI-) MYRIAD GENETICS INC.

XX Kamb A;

XX WPI; 2000-269915/23.

XX N-PSDB; AAA11165.

XX New mutants of the human multiple tumor suppressor gene, useful as  
PT diagnostic markers of cancer, contain specific base alterations or  
PT deletions -

XX PS Disclosure; Column 61-62; 72pp; English.

XX CC The invention relates to variants (AA11196-A11206) of the human

CC multiple tumour suppressor 1 (MTS1) protein of which this sequence

CC represents the wild type sequence. The variants have the following

CC changes relative to the wild type coding sequence: A at any of positions

CC 265, 442, 330 and 329; T at any of positions 172, 238, 341 and 148 and

CC deletions of nucleotides 290-294, 172-179 or 128-129. The variants are

CC somatic mutations of MTS1, indicative of predisposition to melanoma and

CC many other cancers, so detecting them is useful for diagnosis, prognosis

CC and monitoring of cancer (including prenatal analysis). Cells and

CC animals that express the variants are useful as model systems for

CC identifying potential anticancer agents.

XX SQ Sequence 156 AA;

Query Match 98.6%; Score 789; DB 21; Length 156;

Best Local Similarity 98.7%; Pred. No. 8.9e-85;

Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDPAAAGSMPEPSADWLATAAARGVEEVRLLEAVLPNAPNSYGRRPQVMMGMSARVA 60

Db 1 mepaagssmepsadwlataaargveevrllleagalpnapnsygrripqvmmmgsarva 60

QY 61 ELLLLHGAEPNCADPATLTTRPVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAE 120

Db 61 ellllhgaepncadpatltrpvhdaregfdltlvvlhragardvdrdawgrlpvdlae 120

QY 121 LGHRDVARYLRAAAGTGRGSHARIDAAEGPSDIPD 156

Db 121 lghrdvarylraaagtrgsharidaaegpsdipd 156

RESULT 14

AAV91102

ID AAV91102 standard; Protein; 156 AA.

XX AC AAV91102;

XX DT 12-SEP-2000 (first entry)

XX DE Human multiple tumour suppressor MTS1 SEQ ID NO:2.

XX KW Human; multiple tumour suppressor; MTS; somatic mutation; cancer;

XX KW diagnosis; germ line mutation; gene therapy; cytostatic; melanoma;

XX KW leukaemia; astrocytoma; glioblastoma; lymphoma; glioma;

XX KW Hodgkin's lymphoma.

OS Homo sapiens.

XX PN US6060301-A.

XX PD 09-MAY-2000.

XX PF 14-JUL-1998; 98US-0115252.

XX PR 07-JUN-1995; 95US-0480810.

XX PR 08-DEC-1997; 97US-0986147.

XX PR 18-MAR-1994; 94US-0214582.

XX PR 18-MAR-1994; 94US-0215086.

XX PR 18-MAR-1994; 94US-0215087.

XX PR 14-APR-1994; 94US-0227369.

XX PR 01-JUN-1994; 94US-0251938.

XX PR 17-MAR-1995; 95WO-US03316.

XX PA (MYRI-) MYRIAD GENETICS INC.

XX PI Kamb A;

XX WPI; 2000-349676/30.

DR N-PSDB; AAA39353.

XX PT New vector useful for gene therapy of cancer associated with mutation

PT in tumor suppressor gene, comprises DNA sequence of multiple tumor

PT suppressor gene -

XX Disclosure; Column 63-64; 71pp; English.

XX The present invention describes a vector (I) comprising an isolated DNA

CC sequence of a multiple tumour suppressor (MTS) gene having a

CC polynucleotide sequence of the human MTS1E1-beta. (I) is useful for

CC introducing wild-type MTS function to a cancerous or pre-cancerous cell

CC which carries diminished or mutant MTS alleles for suppressing

CC neoplastic growth of the recipient cells. (I) is also useful for

CC increasing the level of expression of MTS gene even in tumour cells in

CC which the mutant gene is expressed at a normal level but the gene

CC product is not fully functional. A host cell transformed with (I) is

CC useful as a model system to study cancer remission and drug treatment

CC which promotes such remission. The present invention relates to somatic

CC mutations and germ line mutations in the MTS gene and their use in the

CC diagnosis and prognosis of human cancer e.g. melanoma, leukaemia,

CC astrocytoma, glioblastoma, lymphoma, glioma, Hodgkin's lymphoma, and

CC cancers of the pancreas, breast, thyroid, ovary, uterus, testis, kidney,

CC stomach and rectum. The present sequence represents human MTS1, which is

CC used in the exemplification of the present invention.

XX SQ Sequence 156 AA;

Query Match 98.6%; Score 789; DB 21; Length 156;

Best Local Similarity 98.7%; Pred. No. 8.9e-85;

Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDPAAAGSMPEPSADWLATAAARGVEEVRLLEAVLPNAPNSYGRRPQVMMGMSARVA 60

Db 1 mepaagssmepsadwlataaargveevrllleagalpnapnsygrripqvmmmgsarva 60

QY 61 ELLLLHGAEPNCADPATLTTRPVHDAAREGFLDTLVVLRHAGARLDVDRDAGRLPVDLAE 120

Db 61 ellllhgaepncadpatltrpvhdaregfdltlvvlhragardvdrdawgrlpvdlae 120

QY 121 LGHRDVARYLRAAAGTGRGSHARIDAAEGPSDIPD 156

Db 121 lghrdvarylraaagtrgsharidaaegpsdipd 156

RESULT 15

AAV59415

ID AAV59415 standard; Protein; 156 AA.

XX AC AAV59415;

XX DT 21-MAR-2000 (first entry)

XX DE Human MTS1 protein sequence.

XX KW MTS; human; polymorphism detection; cancer predisposition; astrocytoma;

XX KW Multiple Tumour Suppressor gene; melanoma; leukaemia; glioblastoma;

XX KW lymphoma; glioma; Hodgkin's lymphoma; chronic lymphocytic leukaemia;

XX KW therapy; MTS1.

OS Homo sapiens.

XX PN US5989815-A.

XX PD 23-NOV-1999.

XX PF 29-APR-1997; 97US-0848251.

XX PR 07-JUN-1995; 95US-0474083.

XX PR 18-MAR-1994; 94US-0214582.

XX PR 18-MAR-1994; 94US-0215086.

XX PR 18-MAR-1994; 94US-0215087.

XX PR 14-APR-1994; 94US-0227369.

Wed Oct 31 07:17:16 2001

us-09-016-869a-2.rag

PR 01-JUN-1994; 94US-0251938.  
PR 17-MAR-1995; 95WO-US03537.  
XX  
PA (UTAH ) UNIV UTAH RES FOUND.  
PA (MYRI-) MYRIAD GENETICS INC.  
XX  
PI Skolnick MH, Cannon-Albright LA, Kamb A;  
XX  
XX WPI: 2000-070785/06.  
DR N-PSDB; AAZ48770.  
XX  
PT Diagnosing a polymorphism associated with a predisposition for cancer -  
XX  
XX Claim 1; Column 61-64; 74pp; English.  
XX  
XX This sequence represents the human MTS1 protein.  
CC The invention relates to a method for diagnosing a polymorphism  
CC associated with a predisposition to cancer by detecting a germ-line  
CC alteration of a wild-type Multiple Tumour Suppressor (MTS) gene or its  
CC expression products in a human sample. The method comprises detecting a  
CC germ-line alteration of a wild-type MTS gene or its expression products  
CC in a human sample, the alteration indicating a predisposition to at least  
CC one of the cancers. The cancer is selected from melanoma, leukaemia,  
CC astrocytoma, glioblastoma, lymphoma, glioma, Hodgkin's lymphoma, breast,  
CC chronic lymphocytic leukaemia (CLL), and cancers of the pancreas, breast,  
CC thyroid, ovary, uterus, testis, kidney, stomach and rectum. The method  
CC may be used as the basis for developing very important diagnostic tests  
CC capable of predicting the predisposition to cancer. The MTS gene is  
CC involved in the progression of multiple tumour types and may provide  
CC means for a general anti-cancer therapy by virtue of its ability to  
CC suppress tumour growth.  
XX  
XX Sequence 156 AA;

Query Match 98.6%; Score 789; DB 21; Length 156;  
Best Local Similarity 98.7%; Pred. No. 8.9e-85;  
Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MDPAGSSMEPSADWLATAAARGVEEVRALEAVALPNAPNSYGRPIQVMMGVSARVA 60  
Db :|||||  
Db 1 mepaagssmepsadwlataaargveevrallleagelpnapnsygrpiqvmmgvsarva 60  
QY 61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAE 120  
Db :|||||  
Db 61 ellllhgaepncadpatltrpvhdaaregfldtlvvlrharldvrdawgrlpvdlace 120  
QY 121 Lghrdvarylraaaggrgsnharidaaegpsdipd 156  
Db :|||||  
Db 121 lghrdvarylraaaggrgsnharidaaegpsdipd 156

Search completed: October 31, 2001, 07:03:38  
Job time: 65 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 31, 2001, 07:02:33 ; Search time 54.92 Seconds  
(without alignments)  
58.487 Million cell updates/sec

Title: US-09-016-869A-2  
Perfect score: 800  
Sequence: 1 MDPAGSSMEPSADWLATAA.....TRGSNHARIDAAGPSDIPD 156

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

1 number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /cgn2.6/prodata/1/1aa/6A-COMB.pep:\*  
4: /cgn2.6/prodata/1/1aa/6B-COMB.pep:\*  
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6: /cgn2.6/prodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	800	100.0	156	2	US-08-627-610-2
2	800	100.0	156	2	US-08-306-511A-2
3	800	100.0	156	2	US-08-893-274-2
4	800	100.0	156	3	US-08-581-918A-2
5	800	100.0	156	4	US-08-346-147B-2
6	800	100.0	156	4	US-08-822-936-2
7	800	100.0	156	5	PCT-US95-04636-2
8	789.5	98.7	157	5	PCT-US96-05252-5
9	789	98.6	156	1	US-08-474-177-2
10	789	98.6	156	1	US-08-487-033-2
11	789	98.6	156	1	US-08-480-810-2
12	789	98.6	156	2	US-08-508-735-2
13	789	98.6	156	2	US-08-848-251-2
14	789	98.6	156	2	US-08-486-047-2
15	789	98.6	156	3	US-09-120-130-2
16	789	98.6	156	3	US-09-115-252-2
17	789	98.6	156	3	US-08-986-515-2
18	789	98.6	156	4	US-09-120-128-2
19	789	98.6	156	4	US-09-120-129-2
20	789	98.6	156	4	US-09-201-139-2
21	789	98.6	156	4	US-09-120-131-2
22	789	98.6	156	4	US-08-910-722-2
23	785	98.1	391	1	US-08-589-981-2
24	760	95.0	148	1	US-08-154-915-4
25	760	95.0	148	3	US-08-384-106A-16
26	760	95.0	148	3	US-08-384-106A-24
27	760	95.0	148	5	PCT-US93-09945-4

28	667.5	83.4	157	3	US-08-581-918A-12	Sequence 12, Appl
29	667.5	83.4	157	4	US-08-346-147B-12	Sequence 12, Appl
30	544	68.0	105	1	US-08-474-177-14	Sequence 14, Appl
31	544	68.0	105	1	US-08-487-033-14	Sequence 14, Appl
32	544	68.0	105	1	US-08-480-810-14	Sequence 14, Appl
33	544	68.0	105	2	US-08-508-735-14	Sequence 14, Appl
34	544	68.0	105	2	US-08-848-251-14	Sequence 14, Appl
35	544	68.0	105	2	US-08-486-047-14	Sequence 14, Appl
36	544	68.0	105	3	US-09-120-130-14	Sequence 14, Appl
37	544	68.0	105	3	US-09-115-252-14	Sequence 14, Appl
38	544	68.0	105	3	US-08-986-515-14	Sequence 14, Appl
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41	544	68.0	105	4	US-09-201-139-14	Sequence 14, Appl
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43	533	66.6	130	2	US-08-627-610-8	Sequence 8, Appl
44	533	66.6	130	3	US-08-581-918A-8	Sequence 8, Appl
45	533	66.6	130	4	US-08-346-147B-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1  
US-08-627-610-2  
; Sequence 2, Application US/08627610  
; Patent No. 5919997  
; GENERAL INFORMATION:  
; APPLICANT: Beach, David H.  
; APPLICANT: Serrano, Manuel  
; APPLICANT: Depinho, Ronald A.  
; TITLE OF INVENTION: Transgenic Animals Having Modified Cell-Cycle  
; TITLE OF INVENTION: Regulation  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 60 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII(text)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/627,610  
; FILING DATE: 04-APR-1996  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Vincent, Matthew P.  
; REGISTRATION NUMBER: 36,709  
; REFERENCE/DOCKET NUMBER: CSI-001CP6  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 156 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-627-610-2

Query Match 100.0%; Score 800; DB 2; Length 156;  
Best Local Similarity 100.0%; Pred. No. 1.6e-87;  
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 MDPAGSSMEPSADWLATAAARGVEEVRALEAVALPNAFNSYGRPIQVMMGSRVA 60  
Db 1 MDPAGSSMEPSADWLATAAARGVEEVRALEAVALPNAFNSYGRPIQVMMGSRVA 60

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QY 61 ELLLLHGAEPNCADPATLTRPVHDAAREGFDTLVVLRHAGARLDVRDAGRLPVDLAE 120
|||||
Db 61 ELLLLHGAEPNCADPATLTRPVHDAAREGFDTLVVLRHAGARLDVRDAGRLPVDLAE 120
|||||
QY 121 LGRDVARYLRAAAGTGRSGNHARIDAAEGPSDIPD 156
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Db 121 LGRDVARYLRAAAGTGRSGNHARIDAAEGPSDIPD 156
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RESULT 2
US-08-306-511A-2
; Sequence 2, Application US/08306511A
; Patent No. 5962316
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Hannon, Gregory J.
; TITLE OF INVENTION: Cell-Cycle Regulatry Proteins, and Uses
; TITLE OF INVENTION: Cell-Cycle Regulatry Proteins, and Uses
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/306,511A
; FILING DATE: 14-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: CSI-001CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 156 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-306-511A-2

Query Match 100.0%; Score 800; DB 2; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.6e-87;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPAAGSSMEPSADWLATAAARGVEEVRALEVALPNAPNSYGRRPQVMMGSRVA 60
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Db 1 MDPAAGSSMEPSADWLATAAARGVEEVRALEVALPNAPNSYGRRPQVMMGSRVA 60
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QY 61 ELLLLHGAEPNCADPATLTRPVHDAAREGFDTLVVLRHAGARLDVRDAGRLPVDLAE 120
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Db 61 ELLLLHGAEPNCADPATLTRPVHDAAREGFDTLVVLRHAGARLDVRDAGRLPVDLAE 120
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QY 121 LGRDVARYLRAAAGTGRSGNHARIDAAEGPSDIPD 156
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Db 121 LGRDVARYLRAAAGTGRSGNHARIDAAEGPSDIPD 156
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RESULT 3
US-08-893-274-2
; Sequence 2, Application US/08893274
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; Patent No. 5968821
; GENERAL INFORMATION:
; APPLICANT: Beach, David H.
; APPLICANT: Demetrick, Douglas J.
; APPLICANT: Serrano, Manuel
; APPLICANT: Hannon, Gregory J.
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins,
; TITLE OF INVENTION: and Uses Related Thereto
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/893,274
; FILING DATE: 15-JULY-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/306,511
; FILING DATE: 14-SEPTEMBER-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/248,812
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,371
; FILING DATE: 14-APRIL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/154,915
; FILING DATE: 18-NOVEMBER-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/991,997
; FILING DATE: 17-DECEMBER-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/963,308
; FILING DATE: 16-OCTOBER-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-071.09
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1000
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 156 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-893-274-2

Query Match 100.0%; Score 800; DB 2; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.6e-87;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPAAGSSMEPSADWLATAAARGVEEVRALEVALPNAPNSYGRRPQVMMGSRVA 60
|||||
Db 1 MDPAAGSSMEPSADWLATAAARGVEEVRALEVALPNAPNSYGRRPQVMMGSRVA 60
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QY 61 ELLLLHGAEPNCADPATLTRPVHDAAREGFDTLVVLRHAGARLDVRDAGRLPVDLAE 120
|||||
Db 61 ELLLLHGAEPNCADPATLTRPVHDAAREGFDTLVVLRHAGARLDVRDAGRLPVDLAE 120
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QY 121 LGRDVARYLRAAAGTGRSGNHARIDAAEGPSDIPD 156
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Db 121 LGRDVARYLRAAAGGTRGNSNHARIDAAGPSDIPD 156

RESULT 4  
US-08-581-918A-2  
; Sequence 2, Application US/08581918A  
; Patent No. 6043030  
; GENERAL INFORMATION:  
; APPLICANT: Beach, David H.  
; APPLICANT: Demetrick, Douglas J.  
; APPLICANT: Serrano, Manuel  
; APPLICANT: Hannon, Gregory J.  
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses  
; TITLE OF INVENTION: Related Thereto  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley, Hoag & Eliot  
; STREET: One Post Office Square  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Wordpad  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/581,918A  
; FILING DATE: 02-JAN-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/497,214  
; FILING DATE: 30-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/346,147  
; FILING DATE: 29-NOV-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/306,511  
; FILING DATE: 14-SEP-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/248,812  
; FILING DATE: 25-MAY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/227,371  
; FILING DATE: 14-APR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/154,915  
; FILING DATE: 18-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/991,997  
; FILING DATE: 17-DEC-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Vincent, Matthew P.  
; REGISTRATION NUMBER: 36,709  
; REFERENCE/DOCKET NUMBER: MIV-071.06  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 832-1299  
; TELEFAX: (617) 832-7000  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 156 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-581-918A-2

Query Match 100.0%; Score 800; DB 3; Length 156;  
Best Local Similarity 100.0%; Pred. No. 1.6e-87;  
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPAGSSMEPSADWLATAAARGVEVRALLEVALPNAPNSYGRRP1QVMMGSRVA 60

Db 1 MDPAGSSMEPSADWLATAAARGVEVRALLEVALPNAPNSYGRRP1QVMMGSRVA 60  
QY 61 ELLLLHCAPNCADPATLTTPVHDAAREGFDTLVVLHAGARLDYRDAGRLPVDLAE 120  
Db 61 ELLLLHGAEPNCADPATLTTPVHDAAREGFDTLVVLHAGARLDYRDAGRLPVDLAE 120  
QY 121 LGRDVARYLRAAAGGTRGNSNHARIDAAGPSDIPD 156  
Db 121 LGRDVARYLRAAAGGTRGNSNHARIDAAGPSDIPD 156

RESULT 5  
US-08-346-147B-2  
; Sequence 2, Application US/08346147B  
; Patent No. 6211334  
; GENERAL INFORMATION:  
; APPLICANT: Beach, David H.  
; APPLICANT: Demetrick, Douglas J.  
; APPLICANT: Serrano, Manuel  
; APPLICANT: Hannon, Gregory J.  
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses  
; TITLE OF INVENTION: Related Thereto  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley, Hoag & Eliot  
; STREET: One Post Office Square  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Wordpad  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/346,147B  
; FILING DATE: 29-NOV-1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/306,511  
; FILING DATE: 14-SEP-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/248,812  
; FILING DATE: 25-MAY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/227,371  
; FILING DATE: 14-APR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/154,915  
; FILING DATE: 18-NOV-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/991,997  
; FILING DATE: 17-DEC-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Vincent, Matthew P.  
; REGISTRATION NUMBER: 36,709  
; REFERENCE/DOCKET NUMBER: MIV-071.04  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 832-1299  
; TELEFAX: (617) 832-7000  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 156 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-346-147B-2

Query Match 100.0%; Score 800; DB 4; Length 156;  
Best Local Similarity 100.0%; Pred. No. 1.6e-87;

Matches	156;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
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Qy	1	MDPAAGSSWEPSADWLATAAARGVEVEVALLAEVALPNAPNSYGRPPTQVMMMGSA	60
Db	1	MDPAAGSSWEPSADWLATAAARGVEVEVALLAEVALPNAPNSYGRPPTQVMMMGSA	60
Qy	61	ELLLHGAEPNCADPATLTPRVHDAAREGFLDPLVYLHAGARLDRVDAWGRLPVDLAE	120
Db	61	ELLLHGAEPNCADPATLTPRVHDAAREGFLDPLVYLHAGARLDRVDAWGRLPVDLAE	120
Qy	121	LGHDRVARYLRAAAGGTGRGSNHARIDAAEGPSDIPD	156
Db	121	LGHDRVARYLRAAAGGTGRGSNHARIDAAEGPSDIPD	156

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RESULT 6
US-08-822-936-2
; Sequence 2, Application US/08822936
; Patent No. 6242575
; GENERAL INFORMATION:
; APPLICANT: Massague, Joan
; APPLICANT: Roberts, James M.
; APPLICANT: Koff, Andrew
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: Isolated P27 Protein, Nucleic Acid
; TITLE OF INVENTION: Molecules Encoding Same, Methods of Identifying Agents Acting
; TITLE OF INVENTION: and Uses of Said Agents
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot, LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/822,936
; FILING DATE: 21-FEBRUARY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-079.05
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 832-1000
; TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 156 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-822-936-2

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Query Match      100.0%; Score 800; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 1.6e-87;
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	1	MDPAAGSMPEPSADWLATAAARGVSEVRALLEAVLPNAPNSYGRRP	QVMMMG	SARVA	60
Db	1	MDPAAGSMPEPSADWLATAAARGVSEVRALLEAVLPNAPNSYGRRP	QVMMMG	SARVA	60
Qy	61	ELLLLHGAEPNCADPATLTPRVHDAAREGFLDTLVVHLRAGARLDV	DWGRLP	VDLAAE	120
Db	61	ELLLLHGAEPNCADPATLTPRVHDAAREGFLDTLVVHLRAGARLDV	DWGRLP	VDLAAE	120
Qy	121	LGHDRVARYRAAAGGTGRGSNHARIDAAEGPSIPD	156		

121 LGHRDVARYLRAAGTRCSNHARIDAAEGPSDIPD 156

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RESULT      7
PCT-US95-04636-2
; Sequence 2, Application PC/TUS9504636
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
; TITLE OF INVENTION: Related Thereto
; NUMBER OF SEQUENCES: 10
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Ascii(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04636
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/346,147
; FILING DATE: 29-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/306,511
; FILING DATE: 14-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/248,812
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,371
; FILING DATE: 14-APR-1994
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 156 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-04636-2

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Query Match 100.0%; Score 800; DB 5; Length 156;  
Best Local Similarity 100.0%; Pred. No. 1.6e-87;  
Matches 156; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MDPAAGSSWEPSADWLATAAARGVEVSRALLPAVALPNAPNSYGRRIQYMMMGSRARVA	60
Db	1	MDPAAGSSWEPSADWLATAAARGVEEVSRALLPAVALPNAPNSYGRRIQYMMMGSRARVA	60
Qy	61	ELLHLGAEPCNCPATLITRVHDDAAREGLDPLVYLHAGARLDVRDAGRLPVDLAAE	120
Db	61	ELLHLGAEPCNCPATLITRVHDDAAREGLDPLVYLHAGARLDVRDAGRLPVDLAAE	120
Qy	121	LGHRDVARYLRAAAGGTGSGNHARIDAAEGPSDIPD	156
Db	121	LGHRDVARYLRAAAGGTGSGNHARIDAAEGPSDIPD	156

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RESULT      8
PCT-US96-05252-5
; Sequence 5, Application PC/TUS9605252
; GENERAL INFORMATION:
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; APPLICANT:
;
; TITLE OF INVENTION:  pl9: A Cell Cycle Inhibitor
;
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  Townsend and Townsend and Crew
; STREET:  One Market Plaza, Steuart Street Tower
; CITY:  San Francisco
; STATE:  California
; COUNTRY:  USA
; ZIP:  94105-1492
; COMPUTER READABLE FORM:

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1  LT      9
2  US-08-474-177-2
3  ; Sequence 2, Application US/08474177
4  ; Patent No. 5624819
5  ; GENERAL INFORMATION:
6  ; APPLICANT: Skolnick, Mark H.
7  ; APPLICANT: Cannon-Albright, Lisa A.
8  ; APPLICANT: Kamb, Alexander
9  ; TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE
10 ; NUMBER OF SEQUENCES: 36
11 ; CORRESPONDENCE ADDRESS:
12 ; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
13 ; STREET: 1201 New York Avenue, Suite 1000
14 ; CITY: Washington
15 ; STATE: DC
16 ; COUNTRY: USA
17 ; ZIP: 20005
18 ; COMPUTER READABLE FORM:
19 ;   MEDIAN TYPE: Floppy disk
20 ;   COMPUTER: IBM PC Compatible
21 ;   OPERATING SYSTEM: PC-DOS/MS-DOS
22 ;   SOFTWARE: PatentIn Release #1.0, Version #1.30
23 ;   CURRENT APPLICATION DATA:
24 ;   APPLICATION NUMBER: US/08/474,177

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RESULT 10
US-08-487-033-2
; Sequence 2, Application US/08487033
; Patent No. 5739027
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS1E1-Beta GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0. Version #1.30

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;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/487,033  
;; FILING DATE: 07-JUN-1995  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US95/03316  
;; FILING DATE: 17-MAR-1995  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/251,938  
;; FILING DATE: 01-JUN-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/215,087  
;; FILING DATE: 18-MAR-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/215,086  
;; FILING DATE: 18-MAR-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/227,369  
;; FILING DATE: 14-APR-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/214,582  
;; FILING DATE: 18-MAR-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Ihnen, Jeffrey L.  
;; REGISTRATION NUMBER: 28,957  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-962-4810  
;; TELEFAX: 202-962-8300  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 156 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;;  
US-08-487-033-2

Query Match 98.6%; Score 789; DB 1; Length 156;  
Best Local Similarity 98.7%; Pred. No. 3.3e-86;  
Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 MDPAGSSMEPSADWLATAAARGVEEVRLLEAVALPNAPNSYGRRPQVMMGSAARVA 60  
Db 1 MDPAGSSMEPSADWLATAAARGVEEVRLLEAVALPNAPNSYGRRPQVMMGSAARVA 60  
  
QY 61 ELLLLHGAEPNCADPATLTTPVHDAAREGFDTLVVLRHAGARLDVDAWGRLPVDLAE 120  
61 ELLLLHGAEPNCADPATLTTPVHDAAREGFDTLVVLRHAGARLDVDAWGRLPVDLAE 120  
  
QY 121 LGRDVARVLRRAAGTGRGSHARIDAAGPSDIPD 156  
Db 121 LGRDVARVLRRAAGTGRGSHARIDAAGPSDIPD 156

RESULT 11  
US-08-480-810-2  
; Sequence 2, Application US/08480810  
; Patent No. 5801236  
; GENERAL INFORMATION:  
; APPLICANT: Kamb, Alexander  
; TITLE OF INVENTION: MTS1 GENE  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
; STREET: 1201 New York Avenue, Suite 1000  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; \*ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/480,810  
;; FILING DATE: 07-JUN-1995  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US95/03316  
;; FILING DATE: 17-MAR-1995  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/251,938  
;; FILING DATE: 01-JUN-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/215,087  
;; FILING DATE: 18-MAR-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/215,086  
;; FILING DATE: 18-MAR-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/227,369  
;; FILING DATE: 14-APR-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/214,582  
;; FILING DATE: 18-MAR-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Ihnen, Jeffrey L.  
;; REGISTRATION NUMBER: 28,957  
;; REFERENCE/DOCKET NUMBER: 24884-109348  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-962-4810  
;; TELEFAX: 202-962-8300  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 156 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;;  
US-08-480-810-2

Query Match 98.6%; Score 789; DB 1; Length 156;  
Best Local Similarity 98.7%; Pred. No. 3.3e-86;  
Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 MDPAGSSMEPSADWLATAAARGVEEVRLLEAVALPNAPNSYGRRPQVMMGSAARVA 60  
Db 1 MDPAGSSMEPSADWLATAAARGVEEVRLLEAVALPNAPNSYGRRPQVMMGSAARVA 60  
  
QY 61 ELLLLHGAEPNCADPATLTTPVHDAAREGFDTLVVLRHAGARLDVDAWGRLPVDLAE 120  
61 ELLLLHGAEPNCADPATLTTPVHDAAREGFDTLVVLRHAGARLDVDAWGRLPVDLAE 120  
  
QY 121 LGRDVARVLRRAAGTGRGSHARIDAAGPSDIPD 156  
Db 121 LGRDVARVLRRAAGTGRGSHARIDAAGPSDIPD 156

RESULT 12  
US-08-508-735-2  
; Sequence 2, Application US/08508735  
; Patent No. 5843756  
; GENERAL INFORMATION:  
; APPLICANT: Stone, Steven  
; APPLICANT: Jiang, Ping  
; APPLICANT: Kamb, Alexander  
; TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF  
; NUMBER OF SEQUENCES: 47  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
; STREET: 1201 New York Avenue, Suite 1000  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA

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;
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/508/735
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US to be assigned
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Innen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348
; TELEPHONE: 202-962-4848
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 156 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-508-735-2

Query Match          98.6%; Score 789; DB 2; Length 156;
Best Local Similarity 98.7%; Pred. No. 3.3e-86;
Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MDPAGSSMEPSADWLATAAARGVEEVRALEAVLPNAPNSYGRRPQVMMMGSAARVA 60
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Db 1 MEPAAGSSMEPSADWLATAAARGVEEVRALEAGALPNAPNSYGRRPQVMMMGSAARVA 60

Qy 61 ELLLLHGAEPNCADPATLTPRPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAE 120
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Db 61 ELLLLHGAEPNCADPATLTPRPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAE 120

Qy 121 LGRDVARYLRAAAGGTGRGSHARIDAAREGSDIPD 156
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Db 121 LGRDVARYLRAAAGGTGRGSHARIDAAREGSDIPD 156

LT 13
US-08-848-251-2
; Sequence 2, Application US/08848251
; Patent No. 5989815
; GENERAL INFORMATION:
; APPLICANT: Skolnick, Mark H.
; APPLICANT: Cannon-Albright, Lisa A.
; TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE AND
; TITLE OF INVENTION: METHOD FOR DETECTING PREDISPOSITION TO CANCER AT THE MTS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/848,251
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/474,083
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: PCT/US95/03537
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Innen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-4810
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 156 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-848-251-2

Query Match          98.6%; Score 789; DB 2; Length 156;
Best Local Similarity 98.7%; Pred. No. 3.3e-86;
Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MDPAGSSMEPSADWLATAAARGVEEVRALEAVLPNAPNSYGRRPQVMMMGSAARVA 60
   |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MEPAAGSSMEPSADWLATAAARGVEEVRALEAGALPNAPNSYGRRPQVMMMGSAARVA 60

Qy 61 ELLLLHGAEPNCADPATLTPRPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAE 120
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Db 61 ELLLLHGAEPNCADPATLTPRPVHDAAREGFLDTLVVLRHAGARLDVRDAGRLPVDLAE 120

Qy 121 LGRDVARYLRAAAGGTGRGSHARIDAAREGSDIPD 156
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Db 121 LGRDVARYLRAAAGGTGRGSHARIDAAREGSDIPD 156

RESULT 14
US-08-486-047-2
; Sequence 2, Application US/08486047
; Patent No. 5994095
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS2 GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,047
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03316
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Innen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-8300
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 156 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-486-047-2

Query Match 98.6%; Score 789; DB 2; Length 156;
Best Local Similarity 98.7%; Pred. No. 3.3e-86;
Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDPAGSSMEPSADWLATAAARGVEEVRLLEAVLPNAPNSYGRRPQVMMGSAVA 60
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1 MEPAAGSSMEPSADWLATAAARGVEEVRLLEAGALPNAPNSYGRRPQVMMGSAVA 60

QY 61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVWDAGRLPVDLAE 120
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61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVWDAGRLPVDLAE 120

Db 61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVWDAGRLPVDLAE 120
;|||||

QY 121 LGHROVARYLRAAAGGTGSGNHARIDAAEGPSDIPD 156
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121 LGHROVARYLRAAAGGTGSGNHARIDAAEGPSDIPD 156

Db 121 LGHROVARYLRAAAGGTGSGNHARIDAAEGPSDIPD 156
;|||||

RESULT 15
US-09-120-130-2
; Sequence 2, Application US/09120130
; Patent No. 6037462
; GENERAL INFORMATION:
; APPLICANT: Kamb, Alexander
; TITLE OF INVENTION: MTS1 GENE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
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; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/120,130
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/480,810
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,938
; FILING DATE: 01-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,087
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/215,086
; FILING DATE: 18-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,369
; FILING DATE: 14-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/214,582
; FILING DATE: 18-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Innen, Jeffrey L.
; REGISTRATION NUMBER: 28,957
; REFERENCE/DOCKET NUMBER: 24884-109348
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-8300
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 156 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-120-130-2

Query Match 98.6%; Score 789; DB 3; Length 156;
Best Local Similarity 98.7%; Pred. No. 3.3e-86;
Matches 154; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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1 MEPAAGSSMEPSADWLATAAARGVEEVRLLEAGALPNAPNSYGRRPQVMMGSAVA 60

Db 1 MEPAAGSSMEPSADWLATAAARGVEEVRLLEAGALPNAPNSYGRRPQVMMGSAVA 60
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QY 61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVWDAGRLPVDLAE 120
;|||||
61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVWDAGRLPVDLAE 120

Db 61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLRAGARLDVWDAGRLPVDLAE 120
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QY 121 LGHROVARYLRAAAGGTGSGNHARIDAAEGPSDIPD 156
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121 LGHROVARYLRAAAGGTGSGNHARIDAAEGPSDIPD 156

Db 121 LGHROVARYLRAAAGGTGSGNHARIDAAEGPSDIPD 156
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